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196.	196.	196.	196.	196.	821 196	819 196.	818 196.	817 196.	816 196.	815 196.	814 196.	813 196.	812 196.	811 196.	810 196.	809 196.	196.	807 196.	806 196.	805 Ly6.	100.	196	196.	196.	120.	196	19	200	799 19	798 19	100	707 10	796 19	795 19	794 13	704 10	793 19	132 13	703	791 19	790 19	67 KB/	100	788 19	787 19	19	T	1	1.	10	19	19	19	100	770	778 19	777 19	776 19	775 19	1/4 19	1/3	773	772 19	771 19	170	770 10	769 19	768 19	1	197	197.	/65 LY/.	700	197.	197.	107.	197	761 197.	760 197.	100	197
196.8 21. 196.8 21.	196.8 21.	196.8 21.	196.8 21.	196.8 21.	821 196.8 21.	819 196.8 21.	818 196.8 21.	817 196.8 21.	816 196.8 21.	815 196.8 21.	814 196.8 21.	813 196.8 21.	812 196.8 21.	811 196.8 21.	810 196.8 21.	809 196.8 21.	196.8 21.	807 196.8 21.	806 196.8 21.	805 196.8 21.	196.0 21.	196 9 21	196.8 21.	196.8 21.	130.0 21.	196.8 21	197 21.	107 21.	799 197 21	798 197 21.	197 197 21.	797 197 21	796 197 21.	795 197 21.	794 197 21.	794 197 21	793 197 21.	132 131 21.	700 107 01	791 197 21.	790 197 21.	789 197 21.	100	788 197 21	787 197 21.	197 21.	197 21.	19/ 21.	107 21.	197 31	197 21.	197 21.	197 21.	100 107 21.	770 107 21	778 197 21.	777 197 21.	776 197 21.	775 197 21.	//4 19/ 21.	7/3 13/ 21.	773 107 31	772 197 21.	771 197 21.	170 137 21.	770 197 31	769 197 21.	768 197 21.	100	197.2 21.	197.2 21.	765 197.2 21.	765 107 2 21	197.2 21.	197.2 21.	107.6	197 2 21	761 197.2 2	760 197.2 21.	100 101 0 01	197.2 21.
196.8 21.7 196.8 21.7	196.8 21.7	196.8 21.7	196.8 21.7	196.8 21.7	821 196.8 21.7	830 196.8 21.7	818 196.8 21.7	817 196.8 21.7	816 196.8 21.7	815 196.8 21.7	814 196.8 21.7	813 196.8 21.7	812 196.8 21.7	811 196.8 21.7	810 196.8 21.7	809 196.8 21.7	196.8 21.7	807 196.8 21.7	806 196.8 21.7	805 196.8 Z1./	100.0 01.7	196 8 21 7	196.8 21.7	196.8 21.7	130.0 21.7	196 B 21 7	197 21.7	107 117	799 197 21.7	798 197 21.7	197 197 21.7	707 107 21 7	796 197 21.7	795 197 21.7	794 197 21.7	704 107 21 7	793 197 21.7	132 13/ 21./	700 107 01 7	791 197 21.7	790 197 21.7	789 197 21.7	100	788 197 21 7	787 197 21.7	197 21.7	197 21.7	13/ 21./	107 21.7	107 21 7	197 21.7	197 21.7	197 21.7	100 100 010	770 107 21 7	778 197 21.7	777 197 21.7	776 197 21.7	775 197 21.7	//4 19/ 21./	1/3 13/ 21./	772 107 21 7	772 197 21.7	771 197 21.7	170 197 21.7	770 197 21 7	769 197 21.7	768 197 21.7	100	197.2 21.7	197.2 21.7	/65 19/.2 21./	766 107 2 21 7	197.2 21.7	197.2 21.7	101 0 01 1	197 2 21 7	761 197.2 21.7	760 197.2 21.7	107.6	197.2 21.7
196.8 21.7 78850 4 US-09- 196.8 21.7 78850 4 US-09-	196.8 21.7 78850 4 US-09-	196.8 21.7 78850 4 US-09-	196.8 21.7 78846 4 US-09-	196.8 21.7 78846 4 US-09-	821 196.8 21.7 78846 4 US-09-	819 196.8 21.7 72922 4 US-US-	818 196.8 21.7 715/4 4 US-09-	817 196.8 21.7 70000 3 US-09-	816 196.8 21.7 54878 4 US-09-	815 196.8 21.7 49052 4 US-09-	814 196.8 21.7 43463 4 US-09-	813 196.8 21.7 41618 4 US-09-	812 196.8 21.7 41617 4 US-09-	811 196.8 21.7 35417 4 US-09-	810 196.8 21.7 28325 4 US-09-	809 196.8 21.7 28321 4 US-09-	196.8 21.7 27659 4 US-09-	807 196.8 21.7 19059 4 US-09-	806 196.8 21.7 13948 4 US-09-	805 196.8 21./ 601 4 US-09-	100 0 21 7 601 4 10 00	196 8 21 7 601 4 119-09-	196.8 21.7 601 4 US-09-	196.8 21.7 601 4 US-09-	190.0 21.7 001 4 00-09-	196 B 21 7 601 4 HS-09-	197 21.7 133719 4 US-US-	200 100 21 1 1 2 1 1 0 1 0 1 0 1 0 1 0 1	799 197 21 7 121982 4 IIS-09-	798 197 21.7 121982 4 US-09-	190 191 01. 1 101.00 1 100.00	797 197 21 7 107421 4 IIS-09-	796 197 21.7 77535 4 US-09-	795 197 21.7 77535 4 US-09-	794 197 21.7 77333 4 00-09-	704 107 21 7 77535 4 115-09-	793 197 21.7 66428 4 US-09-	/32 13/ 21./ 03000 % 03-03-	700 107 01 7 65300 4 110-00-	791 197 21.7 60424 4 US-09-	790 197 21.7 56665 4 US-09-	789 197 21.7 449/1 4 US-US-	700 107 21 7 44071 4 10 00	788 197 21 7 44608 4 IIS-09-	787 197 21.7 41639 4 US-09-	197 21.7 39039 4 US-09-	197 21.7 39032 4 US-09-	17/ C1./ 09C#C 1.12 /C1	107 31 7 34549 4 115-09-	197 21 7 34544 4 119-09-	197 21.7 32327 4 US-09-	197 21.7 20610 4 US-09-	197 21.7 18319 4 US-09-	100 101 01 10110 1 00-00-	770 107 21 7 15615 4 116-00-	778 197 21.7 8409 3 US-09-	777 197 21.7 8396 3 US-09-	776 197 21.7 601 4 US-09-	775 197 21.7 601 4 US-09-	//4 19/ 21./ 6U1 4 US-US-	//3 ±3/ 6±./ 60± ± 05-03-	773 107 31 7 601 4 110-00-	772 197 21.7 601 4 US-09-	771 197 21.7 601 4 US-09-	//O 13/ 21./ GOT 3 UG-03-	770 197 21 7 601 4 118-09-	769 197 21.7 601 4 US-09-	768 197 21.7 601 4 US-09-		197.2 21.7 248968 4 US-09-	197.2 21.7 197875 4 US-09-	/65 19/. 2 21. / 92139 th US-US-	765 107 1 17 00100 1 10 00	197.2 21.7 85854 4 US-09-	197.2 21.7 83697 4 US-09-	101 0 01 1 00 00 1 00 00	197 2 21 7 76610 4 115-09-	761 197.2 21.7 62908 4 US-09-	760 197.2 21.7 61461 4 US-09-	100 101 10 101 10 10 100 100 100 100 10	197.2 21.7 41126 4 US-09-
196.8 21.7 78850 4 US-09-949-016 196.8 21.7 78850 4 US-09-949-016	196.8 21.7 78850 4 US-09-949-016	196.8 21.7 78850 4 US-09-949-016	196.8 21.7 78846 4 US-09-949-016	196.8 21.7 78846 4 US-09-949-016	821 196.8 21.7 78846 4 US-09-949-016	020 106 8 21.7 76300 4 TS-09-949-016	10 10 10 11 11 11 11 11 11 11 11 11 11 1	817 196.8 21.7 70000 3 US-09-851-896	816 196.8 21.7 54878 4 US-09-949-016	815 196.8 21.7 49052 4 US-09-949-016	814 196.8 21.7 43463 4 US-09-949-016	813 196.8 21.7 41618 4 US-09-949-016	812 196.8 21.7 41617 4 US-09-949-016	811 196.8 21.7 35417 4 US-09-949-016	810 196.8 21.7 28325 4 US-09-949-016	809 196.8 21.7 28321 4 US-09-949-016	196.8 21.7 27659 4 US-09-949-016	807 196.8 21.7 19059 4 US-09-949-016	806 196.8 21.7 13948 4 US-09-949-016	805 196.8 21./ 601 4 05-09-949-010	100 0 21.7 001 4 00-00-040-010	196 8 21 7 601 4 119-09-949-016	196.8 21.7 601 4 US-09-949-016	196.8 21.7 601 4 US-09-949-016	190.0 21.7 001 4 00-09-949-010	196.8 21.7 601 4 115-09-949-016	197 21.7 133719 4 US-09-949-016	010 - 010 - 01 - 01 - 01 - 01 - 01 - 01	799 197 21 7 121982 4 US-09-949-016	798 197 21.7 121982 4 US-09-949-016	100 101 0: B 101000 1 10 00 010 010	707 107 21 7 107421 4 115-09-949-016	796 197 21.7 77535 4 US-09-949-016	795 197 21.7 77535 4 US-09-949-016	794 137 21.7 7/307 4 00-03-343-010	704 107 21 7 77535 4 115-09-949-016	793 197 21.7 66428 4 US-09-949-016	/32 13/ 41./ 63300 % 00°03-343-010	700 107 01 7 65300 4 116-00-040-016	791 197 21.7 60424 4 US-09-949-016	790 197 21.7 56665 4 US-09-949-016	789 197 21.7 449/1 4 US-U9-949-UIC	700 107 21 7 4071 4 10 00 040 010	788 197 21 7 44608 4 US-09-949-016	787 197 21.7 41639 4 US-09-949-016	197 21.7 39039 4 US-09-949-016	197 21./ 39032 4 US-09-949-010	17 CT. / 34340 4 02-07-343-040	107 21 7 34549 4 115 00 07 010 010	197 21 7 34544 4 115-09-949-016	197 21.7 32327 4 US-09-949-016	197 21.7 20610 4 US-09-949-016	197 21.7 18319 4 US-09-949-016	100 101 01 1 10010 1 10 00 010 010	770 107 21 7 15615 4 116-00-040-016-	778 197 21.7 8409 3 US-09-167-681-	777 197 21.7 8396 3 US-09-328-174A	776 197 21.7 601 4 US-09-949-016-:	775 197 21.7 601 4 US-09-949-016	//4 L9/ 21./ 6UL 4 US-US-949-ULG-	//3 L9/ 6L./ 6CL 3 00-03-343-016-	773 187 21 7 601 4 115-09-949-016-	772 197 21.7 601 4 US-09-949-016-:	771 197 21.7 601 4 US-09-949-016-	//O 15/ 21./ OUT 1 UG-UG-UG-UTG-	770 197 21 7 601 4 119-09-949-016-	769 197 21.7 601 4 US-09-949-016-	768 197 21.7 601 4 US-09-949-016-		197.2 21.7 248968 4 US-09-949-016-:	197.2 21.7 197875 4 US-09-949-016-	/65 19/.4 21./ 92139 % US*US*910*000*.	765 107 3 7 03130 4 10.00.010.606.1	197.2 21.7 85854 4 US-09-949-016-12	197.2 21.7 83697 4 US-09-949-016-16	101 0 01 0 00 00 00 00 00 00 00 00 00 00	197 2 21 7 76610 4 IIS-09-949-016-15	761 197.2 21.7 62908 4 US-09-949-016-17	760 197.2 21.7 61461 4 US-09-949-016-16	100 100 0 01 01 01 01 01 01 01 01 01 01	197.2 21.7 41126 4 US-09-949-016-17
196.8 21.7 78850 4 US-09-949-016-1601 196.8 21.7 78850 4 US-09-949-016-1620	196.8 21.7 78850 4 US-09-949-016-1601	196.8 21.7 78850 4 US-09-949-016-1601	196.8 21.7 78846 4 US-09-949-016-1279	196.8 21.7 78846 4 US-09-949-016-1279	821 196.8 21.7 78846 4 US-09-949-016-1239	819 196.8 21.7 /2992 4 US-09-949-016-1/59	818 196.8 21.7 715/4 4 US-09-949-U16-1358	817 196.8 21.7 70000 3 US-09-851-896-3	816 196.8 21.7 54878 4 US-09-949-016-1225	815 196.8 21.7 49052 4 US-09-949-016	814 196.8 21.7 43463 4 US-09-949-016-1634	813 196.8 21.7 41618 4 US-09-949-016-1468	812 196.8 21.7 41617 4 US-09-949-016-1435	811 196.8 21.7 35417 4 US-09-949-016-1612	810 196.8 21.7 28325 4 US-09-949-016-1662	809 196.8 21.7 28321 4 US-09-949-016-1193	196.8 21.7 27659 4 US-09-949-016-1761	807 196.8 21.7 19059 4 US-09-949-016-1306	806 196.8 21.7 13948 4 US-09-949-016-1302	805 196.8 21./ 501 4 US-09-949-015-15595	100.0 21.7 001 4 00-00-040-010-1000	196 9 21 7 601 4 118-09-949-016-16204	196.8 21.7 601 4 US-09-949-016-10949	196.8 21.7 601 4 US-09-949-016	190.0 61.7 601 4 00-09-949-010-0809	196 8 21 7 601 4 IIS-09-949-016-3209	197 21.7 133719 4 US-09-949-016-1509	000 101 010 101 011 0 010 010 010 010 0	799 197 21 7 121982 4 US-09-949-016-1410	798 197 21.7 121982 4 US-09-949-016-1208	100 101 01 B 101100 1 10 00 010 1010 10	707 107 21 7 107421 A IIS-00-040-016-1553	796 197 21.7 77535 4 US-09-949-016-1428	795 197 21.7 77535 4 US-09-949-016-1428	794 197 21.7 7/307 4 00-09-949-040-1407	794 197 21 7 77535 4 115-09-949-016-1427	793 197 21.7 66428 4 US-09-949-016-1291	192 197 21.7 00000 % 00-00-030-010-1001	763 167 31 7 65300 4 115-00-040-016-1681	791 197 21.7 60424 4 US-09-949-016-1217	790 197 21.7 56665 4 US-09-949-016-1402	789 197 21.7 449/1 4 US-09-949-016-1/04	700 107 21 7 7707 110 00 010 1707	788 197 21.7 44608 4 US-09-949-016-1560	787 197 21.7 41639 4 US-09-949-016-1547	197 21.7 39039 4 US-09-949-016-1646	197 21.7 39032 4 05-09-949-016-1267	17/ 41./ 34340 4 03-03-343-040-4044	107 31 7 34549 4 110-00-040-016-1613	197 21 7 34544 4 115-09-949-016-1268	197 21.7 32327 4 US-09-949-016-1410	197 21.7 20610 4 US-09-949-016-1461	197 21.7 18319 4 US-09-949-016-1744	100 101 101 101 10 10 10 10 10 10 10 10	770 107 21 7 15615 4 116-00-040-016-	778 197 21.7 8409 3 US-09-167-681-	777 197 21.7 8396 3 US-09-328-174A	776 197 21.7 601 4 US-09-949-016-11502	775 197 21.7 601 4 08-09-949-016-11485	//4 LY/ 21./ 6UL 4 US-US-949-ULG-11460	7/3	773 187 21 7 601 4 115-09-949-016-11451	772 197 21.7 601 4 US-09-949-016-11435	771 197 21.7 601 4 US-09-949-016-	//O 19/ 41./ 601 4 06-09-949-016-1140-1	770 197 21 7 601 4 115-09-949-016-11401	769 197 21.7 601 4 US-09-949-016-	768 197 21.7 601 4 US-09-949-016-78179		197.2 21.7 248968 4 US-09-949-016-:	197.2 21.7 197875 4 US-09-949-016-	/65 19/.4 21./ 92139 % US*US*910*000*.	70E 107 1 21 2 00120 A 110:00-010-006-1	197.2 21.7 85854 4 US-09-949-016-1290	197.2 21.7 83697 4 US-09-949-016-1604	101 0 101 0 101 1 10 00 00 010 100 010 100 010 100 010 100 010 100 010 100 010 100 010 100 010 100 010 100 010	197 2 21 7 76610 4 115-09-949-016-1552	761 197.2 21.7 62908 4 US-09-949-016-1	760 197.2 21.7 61461 4 US-09-949-016-1641	100 -040 -040 -040 -040 -040 -040 -040 -	197.2 21.7 41126 4 US-09-949-016-1727
9-949-016-16201 Sequenc 9-949-016-16201 Sequenc	196.8 21.7 78850 4 US-09-949-016-16014 Sequenc	196.8 21.7 78850 4 US-09-949-016-16013 Sequence	196.8 21.7 78846 4 US-09-949-016-12792	196.8 21.7 78846 4 US-09-949-016-12791 Sequenc	821 196.8 21.7 78846 4 US-09-949-016-12396	819 196.8 21.7 76300 4 MS-09-949-016-1/592 Sequence	119 19 21./ /15/4 4 US-09-949-016-119-00 Sequence	817 196.8 21.7 70000 3 US-09-851-896-3 Sequence	816 196.8 21.7 54878 4 US-09-949-016-12255 Sequenc	815 196.8 21.7 49052 4 US-09-949-016-12203 Sequenc	814 196.8 21.7 43463 4 US-09-949-016-16341 S	813 196.8 21.7 41618 4 US-09-949-016-14681 Sequence	812 196.8 21.7 41617 4 US-09-949-016-14356	811 196.8 21.7 35417 4 US-09-949-016-16129	810 196.8 21.7 28325 4 US-09-949-016-16622 Sequence	: 809 196.8 21.7 28321 4 US-09-949-016-11936 Sequenc	196.8 21.7 27659 4 US-09-949-016-17612 Sequenc	807 196.8 21.7 19059 4 US-09-949-016-13061 Sequence	806 196.8 21.7 13948 4 US-09-949-016-13023 Sequence	805 196.8 21.7 501 4 05-09-949-016-169-65 Sequence	107 0 21 7 CO1 4 CO 00 010 10EOVE CONTROL CONT	196 8 21 7 601 4 IIS-09-949-016-162049 Semience	196.8 21.7 601 4 US-09-949-016-109491 Sequence	196.8 21.7 601 4 US-09-949-016-88079	Tage of the Control o	196.8 21 7 601 4 IIS-09-949-016-32095 Semienc	197 21.7 133719 4 US-09-949-016-15092	000 100 101 101110 4 100 00 1011 101100 00 00 00 00 00 00 00	799 197 21.7 121982 4 IIS-09-949-016-14105 Semienc	798 197 21.7 121982 4 US-09-949-016-12085	197 197 197 197 197 197 197 197 197 197	707 107 21 7 107421 4 IIS-09-049-016-15532 Semient	796 197 21.7 77535 4 US-09-949-016-14281 S	795 197 21.7 77535 4 US-09-949-016-14280 S	194 197 21.7 77333 4 00 00 00 00 00 00 00 00 00 00 00 00 0	704 197 21 7 77535 4 IIS-09-949-016-14279 Semient	793 197 21.7 66428 4 US-09-949-016-12917	132 137 21.7 03300 4 03-03-343-010-10013 Geductic	703 107 31 7 65300 A IIS-00-040-016-16813 Semient	791 197 21.7 60424 4 US-09-949-016-12175 Seguence	790 197 21.7 56665 4 US-09-949-016-14026 Se	789 197 21.7 449/1 4 05-09-949-016-17049	300 101 1 1 100 00 010 170 00 00 00 00 00 00 00 00 00 00 00 00 0	788 197 21.7 44608 4 US-09-949-016-15604 Seguence	787 197 21.7 41639 4 US-09-949-016-15471 Se	197 21.7 39039 4 US-09-949-016-16462 S	197 21.7 39032 4 08-09-949-016-12674 sequence	197 61.7 33340 4 00-03-343-040-14044 0-040-1404	107 21 7 24542 4 US-00-040-015-16124 Semiono	197 21 7 34544 4 IIS-09-949-016-12681 Semienc	197 21.7 32327 4 US-09-949-016-14108 Sequenc	197 21.7 20610 4 US-09-949-016-14610	197 21.7 18319 4 US-09-949-016-17446 Sequence	100 101 111 10010 1 10	770 107 21 7 15615 4 113-00-040-016-17221 Semilario	778 197 21.7 8409 3 US-09-167-681-37 Sequence	777 197 21.7 8396 3 US-09-328-174A-1 S	776 197 21.7 601 4 US-09-949-016-115022	775 197 21.7 601 4 US-09-949-016-114854 S	1/4 19/ 21./ 601 4 03-09-949-016-114666 Sequence	1/3 to the first of the second	773 197 21 7 601 4 IIC-09-949-016-114518 Semient	772 197 21.7 601 4 US-09-949-016-114350 S	771 197 21.7 601 4 US-09-949-016-114182	1/0 15/ 61./ GOT 3 CO-CO-CO-CO-CO-CO-CO-CO-CO-CO-CO-CO-CO-C	770 197 21 7 601 4 IIS-09-949-016-114014 Semienc	769 197 21.7 601 4 US-09-949-016-113846	768 197 21.7 601 4 US-09-949-016-78179 Sequence		197.2 21.7 248968 4 US-09-949-016-12614 Seguence	197.2 21.7 197875 4 US-09-949-016-15425 Se	765 197.2 21.7 92139 % US-09-11 Sequence	107 107 1 107 107 107 107 107 107 107 10	197.2 21.7 85854 4 US-09-949-016-12908 Se	197.2 21.7 83697 4 05-09-949-016-16040 86	101 0 01 1 0 01 01 01 01 01 01 01 01 01	197 2 21 7 76610 4 IIS-09-949-016-15521 Semienc	761 197.2 21.7 62908 4 US-09-949-016-17554 Sequence	760 197.2 21.7 61461 4 US-09-949-016-16419 Sequence	1/0 107 0 11 7 14120 4 07 07 040 160 100 00	197.2 21.7 41126 4 US-09-949-016-17273 Sequence

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194.4 21.4 7070 4 US-09- 194.4 21.4 7070 4 US-09- 194.4 21.4 8150 4 US-09- 194.4 21.4 15927 4 US-09- 194.4 21.4 18725 4 US-09- 194.4 21.4 34534 4 US-09- 194.4 21.4 35104 4 US-09- 194.4 21.4 37711 4 US-09-	194.4 21.4 601 4 US-09-194.4 21.4 601 4 US-09-	194.4 21.4 601 4 US-09-	194.6 21.5 529885 4 US-09- 194.6 21.5 529885 4 US-09- 194.6 21.5 529885 4 US-09-	194.6 21.5 529885 4 US-09- 194.6 21.5 529885 4 US-09- 194.6 21.5 529885 4 US-09-	194.6 21.5 529885 4 US-09- 194.6 21.5 529885 4 US-09-	194.6 21.5 529885 4 US-09-	194.6 21.5 529885 4 US-09- 194.6 21.5 529885 4 US-09-	194.6 21.5 529885 4 US-09- 194.6 21.5 529885 4 US-09-	194.6 21.5 524032 4 US-09- 194.6 21.5 524032 4 US-09-	194.6 21.5 524032 4 US-09- 194.6 21.5 524032 4 US-09-	194.6 21.5 524032 4 US-09- 194.6 21.5 524032 4 US-09- 194.6 21.5 524032 4 US-09-	194.6 21.5 151089 4 US-09- 194.6 21.5 524032 4 US-09-	194.6 21.5 137753 4 US-09- 194.6 21.5 147840 4 US-09-	194.6 21.5 120727 4 US-09- 194.6 21.5 132438 4 US-09- 194.6 21.5 132438 4 US-09-	194.6 21.5 99304 4 US-09- 194.6 21.5 120727 4 US-09-	194.6 21.5 72662 4 US-09-	194.6 21.5 /1645 4 US-09-	194.6 21.5 5/50/ 4 US-09-	194.6 21.5 50269 4 US-09-	194.6 21.5 43577 4 US-09-	194.6 21.5 41684 4 US-09- 194.6 21.5 43576 4 US-09-	194.6 21.5 2/412 4 US-09- 194.6 21.5 28109 4 US-09-	194.6 21.5 19167 4 US-09-	194.6 21.5 16236 4 US-09- 194.6 21.5 17328 4 US-09-	194.6 21.5 15019 4 US-09-	194.6 21.5 601 4 US-09-	194.6 21.5 601 4 US-09- 194.6 21.5 601 4 US-09-	194.6 21.5 601 4 US-09- 194.6 21.5 601 4 US-09- 194.6 21.5 601 4 US-09-
194.4 21.4 7070 4 US-09-949-011 194.4 21.4 7070 4 US-09-949-011 194.4 21.4 8150 4 US-09-949-011 194.4 21.4 15927 4 US-09-949-011 194.4 21.4 18725 4 US-09-949-011 194.4 21.4 34534 4 US-09-949-011 194.4 21.4 34534 4 US-09-949-011 194.4 21.4 37711 4 US-09-949-011	194.4 21.4 601 4 US-09-949-011	194.4 21.4 601 4 US-09-949-011 194.4 21.4 601 4 US-09-949-011 194.4 21.4 601 4 US-09-949-011 194.4 21.4 601 1 US-09-949-011 194.4 21.4 601 4 US-09-949-011	194.6 21.5 529885 4 US-09-949-010 194.6 21.5 529885 4 US-09-949-010 194.6 21.5 529885 4 US-09-949-010	194.6 21.5 529885 4 US-09-949-010 194.6 21.5 529885 4 US-09-949-010 194.6 21.5 529885 4 US-09-949-010	194.6 21.5 529885 4 US-09-949-01 194.6 21.5 529885 4 US-09-949-01	194.6 21.5 529885 4 US-09-949-010	194.6 21.5 529885 4 US-09-949-010 194.6 21.5 529885 4 US-09-949-010	194.6 21.5 529885 4 US-09-949-016 194.6 21.5 529885 4 US-09-949-016	194.6 21.5 524032 4 US-09-949-011 194.6 21.5 524032 4 US-09-949-011	194.6 21.5 524032 4 US-09-949-010	194.6 21.5 524032 4 US-09-949-016 194.6 21.5 524032 4 US-09-949-016	194.6 21.5 151089 4 US-09-949-01	194.6 21.5 137753 4 US-09-949-01 194.6 21.5 147840 4 US-09-949-01	194.6 21.5 120727 4 US-09-949-011 194.6 21.5 132438 4 US-09-949-011 194.6 21.5 132438 4 US-09-949-011	194.6 21.5 99304 4 US-09-949-01 194.6 21.5 120727 4 US-09-949-01	194.6 21.5 72662 4 US-09-949-010	194.6 21.5 71651 4 US-09-949-01	194.6 21.5 69701 4 US-09-949-01.	194.6 21.5 50269 4 US-09-949-010	194.6 21.5 43577 4 US-09-949-010	194.6 21.5 41684 4 US-09-536-059	194.6 21.5 2/412 4 US-09-949-016	194.6 21.5 19167 4 US-09-949-016	194.6 21.5 16236 4 US-09-949-016 194.6 21.5 17328 4 US-09-949-016	194.6 21.5 15019 4 US-09-949-016	194.6 21.5 601 4 US-09-949-016	194.6 21.5 601 4 US-09-949-016	194.6 21.5 601 4 US-09-949-016 194.6 21.5 601 4 US-09-949-016 194.6 21.5 601 4 US-09-949-016
194.4 21.4 7070 4 US-09-9 194.4 21.4 7070 4 US-09-9 194.4 21.4 8150 4 US-09-9 194.4 21.4 15927 4 US-09-9 194.4 21.4 18725 4 US-09-9 194.4 21.4 34534 4 US-09-9 194.4 21.4 35104 4 US-09-9 194.4 21.4 37711 4 US-09-9	194.4 21.4 601 4 US-09-949-011	194.4 21.4 601 4 US-09-949-016-18151 194.4 21.4 601 4 US-09-949-016-80629 194.4 21.4 601 4 US-09-949-016-10629 194.4 21.4 601 4 US-09-949-016-10629 194.4 21.4 601 4 US-09-949-016-10629	194.6 21.5 529885 4 US-09-949-010 194.6 21.5 529885 4 US-09-949-010 194.6 21.5 529885 4 US-09-949-010	194.6 21.5 529885 4 US-09-949-010 194.6 21.5 529885 4 US-09-949-010 194.6 21.5 529885 4 US-09-949-010	194.6 21.5 529885 4 US-09-949-01 194.6 21.5 529885 4 US-09-949-01	194.6 21.5 529885 4 US-09-949-010	194.6 21.5 529885 4 US-09-949-010 194.6 21.5 529885 4 US-09-949-010	194.6 21.5 529885 4 US-09-949-016 194.6 21.5 529885 4 US-09-949-016	194.6 21.5 524032 4 US-09-949-011 194.6 21.5 524032 4 US-09-949-011	194.6 21.5 524032 4 US-09-949-010	194.6 21.5 524032 4 US-09-949-016 194.6 21.5 524032 4 US-09-949-016	194.6 21.5 151089 4 US-09-949-01	194.6 21.5 137753 4 US-09-949-01 194.6 21.5 147840 4 US-09-949-01	194.6 21.5 120727 4 US-09-949-011 194.6 21.5 132438 4 US-09-949-011 194.6 21.5 132438 4 US-09-949-011	194.6 21.5 99304 4 US-09-949-01 194.6 21.5 120727 4 US-09-949-01	194.6 21.5 72662 4 US-09-949-010	194.6 21.5 71651 4 US-09-949-01	194.6 21.5 69701 4 US-09-949-01.	194.6 21.5 50269 4 US-09-949-010	194.6 21.5 43577 4 US-09-949-010	194.6 21.5 41684 4 US-09-536-059- 194.6 21.5 43576 4 US-09-949-016-	194.6 21.5 2/412 4 US-09-949-016-	194.6 21.5 19167 4 US-09-949-016-	194.6 21.5 16236 4 US-09-949-016- 194.6 21.5 17328 4 US-09-949-016-	194.6 21.5 15019 4 US-09-949-016-	194.6 21.5 601 4 US-09-949-016-	194.6 21.5 601 4 US-09-949-016-	194.6 21.5 601 4 US-09-949-01 194.6 21.5 601 4 US-09-949-01 194.6 21.5 601 4 US-09-949-01
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194.4 21.4 7070 4 US-09-949-016-12322 Sequence 194.4 21.4 7070 4 US-09-949-016-13322 Sequence 194.4 21.4 8150 4 US-09-949-016-13830 Sequence 194.4 21.4 15927 4 US-09-949-016-12228 Sequence 194.4 21.4 18725 4 US-09-949-016-12228 Sequence 194.4 21.4 18725 4 US-09-949-016-15141 Sequence 194.4 21.4 34534 4 US-09-949-016-15831 Sequence 194.4 21.4 37711 4 US-09-949-016-12832 Sequence	194.4 21.4 601 4 US-09-949-016-109496 Sequence 194.4 21.4 601 4 US-09-949-016-112381 Sequence 194.4 21.4 601 4 US-09-949-016-112380 Sequence 194.4 21.4 601 4 US-09-949-016-189757 Sequence 194.4 21.4 601 4 US-09-949-016-201582 Sequence	194.4 21.4 601 4 US-09-949-016-18151 Sequence 194.4 21.4 601 4 US-09-949-016-80629 Sequence 194.4 21.4 601 4 US-09-949-016-186810 Sequence 194.4 21.4 601 4 US-09-949-016-108810 Sequence 194.4 21.4 601 4 US-09-949-016-108810 Sequence	194.6 21.5 529885 4 US-09-949-016-14346 Sequence 194.6 21.5 529885 4 US-09-949-016-14346 Sequence 194.6 21.5 529885 4 US-09-949-016-14347 Sequence 194.6 21.5 529885 4 US-09-949-016-14347 Sequence 198.6 21.5 529885 4 US-09-949-016-14347 Sequence 2018 529885 4 US-09-949-016-14347	194.6 21.5 529885 4 US-09-949-016-14345 Sequence 194.6 21.5 529885 4 US-09-949-016-14345 Sequence	194.6 21.5 529885 4 US-09-949-016-14343 Sequence: 194.6 21.5 529885 4 US-09-949-016-14344 Sequence: 194.6 21.5 529885 4 US-09-949-016-14344 Sequence:	194.6 21.5 529885 4 US-09-949-016-14342 Sequence 194.6 21.5 529885 4 US-09-949-016-14343 Sequence	194.6 21.5 529885 4 US-09-949-016-14341 Sequence: 194.6 21.5 529885 4 US-09-949-016-14342 Sequence:	194.6 21.5 529885 4 US-09-949-016-14341 Sequence: 194.6 21.5 529885 4 US-09-949-016-14341 Sequence:	194.6 21.5 524032 4 US-09-949-016-16931 Sequence 194.6 21.5 524032 4 US-09-949-016-16931 Sequence 194.6 21.5 524032 4 US-09-949-016-16301 Sequence	194.6 21.5 524032 4 US-09-949-016-16930 Sequence : 194.6 21.5 524032 4 US-09-949-016-16930 Sequence :	194.6 21.5 524032 4 US-09-949-016-16929 Sequence : 194.6 21.5 524032 4 US-09-949-016-16929 Sequence :	194.6 21.5 151089 4 US-09-949-016-14348 Sequence 194.6 21.5 524032 4 US-09-949-016-16928 Sequence	194.6 21.5 137753 4 US-09-949-016-17404 Sequence 194.6 21.5 147840 4 US-09-949-016-15236 Sequence	194.6 21.5 120727 4 US-09-949-016-15-788 Sequence: 194.6 21.5 132438 4 US-09-949-016-14349 Sequence: 194.6 21.5 132438 4 US-09-949-016-14350 Semmence: 194.6 21.5 132438 4 US-09-949-016-14350	194.6 21.5 99304 4 US-09-949-016-15440 Sequence 194.6 21.5 120727 4 US-09-949-016-15787 Sequence	194.6 21.5 73308 4 US-09-949-016-16326 Sequence	194.6 21.5 /1645 4 US-09-949-016-17258 Sequence	194.6 21.5 5/50/ 4 US-09-949-016-14187 Sequence	194.6 21.5 50269 4 US-09-949-016-17598 Sequence	194.6 21.5 43577 4 US-09-949-016-12183 Sequence	194.6 21.5 41684 4 US-09-536-059-1 Seguence :	194.6 21.5 28109 4 US-09-949-016-14329 Sequence:	194.6 21.5 19167 4 US-09-949-016-12432 Sequence	194.6 21.5 16236 4 US-09-949-016-16298 Sequence : 194.6 21.5 17328 4 US-09-949-016-15736 Sequence :	194.6 21.5 15019 4 US-09-949-016-13571 Sequence	194.6 21.5 601 4 US-09-949-016-193400 Sequence 194.6 21.5 10148 4 US-09-949-016-13252 Sequence	194.6 21.5 601 4 US-09-949-016-193214 Sequence 194.6 21.5 601 4 US-09-949-016-193307 Sequence	194.6 21.5 601 4 US-09-949-016-180682 Sequence 194.6 21.5 601 4 US-09-949-016-184669 Sequence 194.6 21.5 601 4 US-09-949-016-1893121 Sequence 194.6 21.5 601 4 US-09-949-016-193121
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US-09-949-016-14632, Application US/09949016

¡ Sequence 14632, Application US/09949016

¡ Batent No. 6812339

¡ GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, MET

FILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOPTWARE: PABESEQ for Windows Version 4.0

SEQ ID NO 14632

LENGTH: 12445

TYPE: DNA
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; FEATURE;
; NAME/KEY: misc_feature
; LOCATION: (1)...(12445)
; OTHER INFORWATION: n = A
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US-09-949-016-12071
US-09-949-016-12011
US-09-949-016-13365
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Sequence 15748, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 15748

LENGTH: 21691
                           ; NAME/KEY: misc feature
; LOCATION: (1)...(21691)
; OTHER INFORMATION: n =
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ORGANISM: Human
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Best Local Similarity 99.9%;
Matches 906; Conservative
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                                                                                                   TGCGGTGAGCCGAGATCGCGCCGCTGATTCCAGCCTGGGCGACAAGAGTGAGACTCCATC
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TCACACA 12071
                                                                        TGCGGTAAGCCGAGATCGCGCCGCTGATTCCAGCCTGGGCGACAAGAGTGAGACTCCATC 12064
                                                                                                                                                     TAGTCCCAGTTACTCGGGAGGCTGAGGCAGGAAAATCGCTTGAACCCAGGAGGCGGACGT
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Goodrich,

Ryle

Y. Tom

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APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: No. 6783965el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REPERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOPTWARE: pt FL genes Version 2.0
SEQ ID NO 204
LENGTH: 1154
TYPE: DNA
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Best Local Similarity
Matches 604; Conserv
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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LOCATION: (409)..(768)
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769
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Xue, Aidong J
Zhao, Qing A
Wang, Jian-Rui
Ma, Yunqing
Yamazaki, Victoria
Chen, Rui-hong
Wang, Zhiwei
                 TAAAACCACAGGGCTGGATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCCAGCAATTCTCA 540
                                                                                      TCTGCCCAGCTCCTCTGCTGCCAGTGGCAGTGGCACGAGGTGGGGCTTTTGTGCCAG 480
                                                                                                                       GGTGGGGGGCGAAACTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCA
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Yang, Yonghong
Wehrman, Tom
 TANANCCACAGGCTGGATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCA
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ng, Jie
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99.3%;
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GENERAL Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Hilman, Jennifer L.
APPLICANT: Hilman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Reddy, Roopa
APPLICANT: Redgler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: 11CYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
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Patent No.
                                                                                                                          Matches
                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/079,677
APPLICATION MARCH 27, 1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lynn E. Murry, Ph.D.
REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA-0008 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650.045356
                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (650) 855-05
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                             TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAITUT07
CLONE: 1506513
                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 500 base pairs
                                                                                                                                                                                                                                                        TYPE: STRANDEDNESS: B1..
                                                                                                                        watch 55.1%; Score 500; DB 3; L
Local Similarity 100.0%; Pred. No. 8.4e-146;
nes 500; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: Herewith
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197 TCAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGACACTTGGCA
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT EPILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOPTWARE: PastSEQ for Windows Version 4.0

**SOPTWARE: PastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                     NAME/KEY: misc_feature; LOCATION: (1)...(160759); OTHER INFORMATION: n = A US-09-949-016-16514
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                                                                                                                                                                                 Matches 263;
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                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 160759
                                                                                                                                                                                                Local Similarity
                                                                                                                            598 ATTAGCAATTAAAACTGAGAAATGGGCCGGGCACGGTGGCTCACGCCTGTAATCCCAGCA
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ACATGGTGAAA--CCTTGTCTACTAAAAATACAAAAAATTAGCCAGGCACAGTGGTGTGC 775
                                                        CTTTGGGAGGCCGAGGCGGGTGGATCACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCA 717
                                                                                                         ATGATAAATTATAAATAGCCTTAAGGCTGGCACGGTGGCTCACGCCTGTAATCCCAGCA
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: MOMENTAL SATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 15377
LENGTH: 23533
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US-09-949-016-15377
Sequence 15377, Application US/09949016
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US-09-949-016-15377
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Best Local Similarity
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                                                                                                                                                                                        CTACTAAAAATACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCAGTTACT
                                                                                                                                                                                                                                                                    GTGGATCACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGT--
                                                                                                                                                                                                                                                                                                                             AAAAAĞGCCGGGCACAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGG
                                                                                                                                                                                                                                                                                                                                                      AAATGGGCCGGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAAGGCCGAGGCCG
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                                                                                                                    CGGGAGGCTGAGGCAGGAAAATCGCTTGAACCCCAGGAGGCGGACGTTGCGGTGAGCCGAG
                                                                                                                                                              CTACTTANAACACAAAAATTAGTTGGGTGTGGTACGCACCTGTAATCCCAGCTACT
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                                                                                CGGGAGGCTGAGGCAGGAGATCATTTGAACCCCAGGAGGCGGATGTTGCAGTGAGCCGAG
ATCGTGCCACTGTACTCCAGCCTGGGGGACAAGAGCGAGACTTCATCTCAAAAA 5831
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78.5%;
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RESULT 7 US-09-949-016-12969 ; Sequence 12969, Application US/09949016

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US-09-949-016-11957/c
, Sequence 11957, Application US/09949016
, Patent NO. 6812319
, GENERAL INFORMATION:
, APPLICANT: VENTER, J. Craig et al.
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US-09-949-016-12969
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GENERAL INFORMATION:
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Best Local
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LENGTH: 36148
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11957
LENGTH: 64813
TYPE: DNA
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

PILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-014-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOPTWARE: FRANCESCO for Windows Version 4.0
                                                                                        APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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Local Similarity 84.7%;
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US-09-949-016-11957
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US-09-949-016-16064
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Best Local Similarity
Matches 272; Conser
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: FOLLMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CLOO1307
CURRENT APPLICATION UNMERE: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16064
LENGTH: 70131
TYPE: DNA
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                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                            Local Similarity 80.
1es 272; Conservative
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                  TCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAA--CCTTGTCTACTAAAAATACAA 749
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                                                                    GGTAGCTCACGCCTGTAATCCCAGCACTTTGGGAGGTTGAGGCGGGGTGGATCACCTGAGG
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Pred. No. 2e
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Pred. No. 2.1e-54;
0; Mismatches 64;
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US-09-949-016-12682
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                                                                      RESULT 11
US-09-949-016-16288
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; ORGANISM: Human
US-09-949-016-12682
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                   Sequence 16288, Application US/09949016 Patent No. 6812339 GENERAL INFORMATION:
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Best Local Similarity
Matches 252; Conser
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SOFTWARE: FRANCEQ for Windows Version 4.0
SEQ ID NO 12682
LENGTH: 63187
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
 APPLICANT:
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o. 6812339
VENTER, J. Craig et al.
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Pred. No. 2.3e-54;
0; Mismatches 51;
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CLOO1307
CURRENT APPLICATION UNMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,488
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FBSUSEQ for Windows Version 4.0
SEQ ID NO 16288
LENGTH: 63187
                                                                                                                                GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OP INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OP INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12786
LENGTH: 35678
TYPE: DNA
ORGANISM: Human
S-09-949-016-12786
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12786, Apparent No. 6812339
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ORGANISM: Human
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52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCAGTTACTCGGGAGGCTGAGGCAGGAAAAATCGCTTGAACCCCAGGAGGCGGACGTTGCG 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAACCCCGTCTACTAAAAATACAAAAAAATTAGTTGGGCATGGTGGCAGGTGCCTGTAAT 9066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09949016
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER

TITLE OF INVENTION WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 16757
                                                                                                                                                                                                                                                                                                                                                                                        ; LENGTH: 35678
; TYPE: DNA
; ORGANISM: Human
; ORGANISM: Human
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US-09-949-016-16757/c
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Best Local Similarity
Matches 247; Conserv
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Patent No. 6812339
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 247; Conserv
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CTATAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCACTGGAACCCAGGAGGTGGA 10022
                                                                                                               ACATGGTGAAACCTTGTCTACTAAAAATACAAAAATTAGCCAGGCACAGTGGTGTGCAC
                              TGGTAGTCCCAGTTACTCGGGAGGCTGAGGCAGGAAAATCGCTTGAACCCCAGGAGGCGGA 837
                                                                           ACATGGTGAAACCTGGTCTACTAAAAATACAAAAAATTAGCTGGGCGTGGTGGCATGCAC
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOCTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16758
LENGTH: 35678
TYPE: DNA
US-09-949-016-16755/c
; Sequence 16755, Application US/09949016
; Patent NO. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
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US-09-949-016-16758/c
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                                                                                                                                                        RESULT 15
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16758, Application US/09949016 Patent No. 6812339
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Best Local Similarity
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FILE REFERENCE: CL001307

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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTMARE: PSSESSEQ FOR WINDOWS Version 4.0
SEQ ID NO 16755
LENGTH: 58361
TYPE: DNA
ORGANISM: Human
US-09-949-016-16755
Search completed: September 15, 2005, 18:28:34
Job time : 327 secs
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9231.094 Million cell updates/sec
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AA399124 zt49a02: x
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BC019875 homo sapi
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190 20.9 624 6 CA416290 190 20.9 660 4 BG771029 190 20.9 694 8 BZ603428 190 20.9 698 1 AV728560 190 20.9 698 1 AV728560	190 20.9 588 7 CN344468 190 20.9 598 4 BF977720 190 20.9 619 8 AQ545078	190 20.9 543 5 BU947622 190 20.9 573 5 BU177705 190 20.9 574 8 AQ820118	190 20.9 529 8 B15895 190 20.9 541 7 CN263446	190 20.9 509 1 AI815210 190 20.9 529 4 BG402924	190 20.9 491 2 AW469214 190 20.9 508 8 AQ418545	190 20.9 479 7 CN276493	190 20.9 466 8 AQ382614	190 20.9 439 2 AW469462 190 20.9 465 1 AA748071	190 20.9 431 1 2015948	190 20.9 420 7 CN277619	190 20.9 414 4 BG112362	190 20.9 390 9 AG192505	190 20.9 385 8 AQ278103	190.2 21.0 1805 3 CR621123 190.2 21.0 1888 3 BC037885	190.2 21.0 1170 3 BC017436	190.2 21.0 1049 1 AL572160 190.2 21.0 1080 5 BQ213854	190.2 21.0 898 5 BU181297	190.2 21.0 871 4 BI856069	190.2 21.0 721 9 AG085756	190.2 21.0 709 9 AG143216	190.2 21.0 706 9 AG113042	190.2 21.0 699 7 CR789789	190.2 21.0 687 1 AI174827	190.2 21.0 672 1 AV648612	190.2 21.0 667 9 AG165154	190.2 21.0 666 9 AG040280	190.2 21.0 663 1 AL709338	190.2 21.0 63/ 8 AQ423458	190.2 21.0 626 9 AG018336	190.2 21.0 613 7 W27084	190.2 21.0 607 9 AG018337	190.2 21.0 601 5 BX504170	190.2 21.0 589 8 AQ041600	190.2 21.0 577 8 B14093	190.2 21.0 570 8 AQ018599	190.2 21.0 566 5 BU957747	190.2 21.0 564 5 BU860291	190.2 21.0 528 8 B55695	190.2 21.0 525 8 AQ082123	190.2 21.0 520 6 CA946754	190.2 21.0 498 7 CR787110	190.2 21.0 490 8 AQ432147	190.2 21.0 477 8 AQ632842	190.2 21.0 4/0 8 AQ226326
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	FEATURES BOURC	COMMENT	REFERENCE AUTHORS TITLE	RESULT 1 CA427660/c LOCUS DEFINITION ACCESSION VERSION VERSION	1485 1486 1486 1487 1488 1489 1499 1491 1492 1492 1493 1495 1495 1497 1499 1499 1500
/organism="Homo sapiens" /mol_type="mRNAM" /db_xref="taxon:9606" /clone="Ul-H-DP0-beo-o-24-0-Ul" /clone="Ul-H-DP0-beo-o-24-0-Ul" /clone="Ul-H-DP0-beo-o-24-0-Ul" /clone="Whilb (Life Technologies)" /clone lib="NC1 CGAP DF0" /clone lib-"NC1 COAP DF0" /clone lib-"NC1 CAP DF0" /clone lib-"	EATURES Bource	2	-	RESULT 1 CA427660/c CA427660 CA427660 DEFINITION UI-H-DF0-beo-o-24-0-UI.81 NCI CGAP_DF0 Homo UI-H-DF0-beo-o-24-0-UI 3', mRNA sequence. ACCESSION CA427660 VERSION CA427660.1 GI:24790386	000000000000000000000000000000000000000

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AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 470)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
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Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-UT0114-301100-358-E10&t3=2000-11-30&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 470.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
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CCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGAC 559
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/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="UT0114"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?tl=IL3&t2=IL3-UT0114-
081200-366-E06&t3=2000-12-08&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 455.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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    GTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGGGGACAGTTCTGTTGTGCTTG
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/mol type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="UT0114"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /notes Torgan: uterus tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: asimpson@ludwig.org.br
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seripts/gethtml2.pl?tl=IL3&t2=IL3-UT0114-
221100-340-G10&t3=2000-11-22&t4=1)
Seq primer: puc 18 forward
Seq primer: puc 18 forward
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1 (bases 1 to 470)
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Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
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                                                                                                                                                                              /organism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dev_stage="Adult"
/dev_stage="Adult"
/clone_lib="UT0114"
/clone_lib="UT0114"
/note="Organ: uterus_tumor; Vector: puc18; Site_1: SmaI;
/note="Torgan: uterus_tumor; Vector: puc18; Site_1: SmaI;
/note="Tor
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99.8%;
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1 (bases 1 to 792)
1 (bases 1 to 792)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                 Plate: NDCM136 row: e column: 18
High quality sequence stop: 462.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
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CB985553.1 GI:30280077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
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adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCAGCAGCAGGCGCGCGCACATGG-1010N-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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6

Length

AAATACAAAAAATTAGCC 759 GCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA-CC GGGAGTGGCACGAGGTGGGGGCTTTTGTGCCAGTAAAACCACAGGCTGGATTTTGCCTGCGGG GGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGACACTTGGCAAGGTCCAGCGATG TGAGATCAGG-AGTTCAAGACCAG-CCTGGCCAACATGGTGAAACCTTGTCT---ACTAA GCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAAGCGGGTGGATCACCC TTTCATTGTATCTATTGATTTTTACCACATTAGCAATTAAAAAACTGAGAAAATGGGCCGG TTTCATTGTATCTATTGATTTTTACCACATTAGCAATTAAAA--CTGAGAAATGGGCCGG CCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGACCCCAAAGAGC CCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGACCCCAAAGAGC GGGAGTGGCACGAGGTGGGGCTTTGTGCCAGTAAAACCACAGGCTGGATTTGCCTGCGGG CCAGAGGGTCTGGGCCCGGCCACAGAGTCATCTGCCCAGCTCCTCTGCTGCTGGCCAGT GTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGGCGCAAACTCCATAAAGAA GTCCGGAGTCCACACACAGACTGGCGGCAGGCAGGAGGGGGACAGTTCTGTTGTGCTTG GGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGACACTTGGCAAGGTCCAGCGATG TGAGATCAGGAAGTTCAAGACCAGCCCTGGCCCAAATGGTGAAAACCTTGGTCTACTTAA Conservative 51.4%; 95.7%; 0; Score 466.4; DB 6 Pred. No. 1.7e-66; Mismatches 16; Indels 8 Gaps 576 741 516 686 456 627 396 569 336 509 276 449 216 389 156 329 96 5

zx80a06.rl Soares ovary tumor NbHOT IMAGE:810034 5', mRNA sequence. 480 bp mRNA Homo sapiens linear CDNA EST 10-JUN-1997 clone

Homo sapiens AA464988 AA464988.1 GI:2189872 sapiens (human)

1 (bases 1 to 480)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G.,
Hillier,L., Allen,M., Le,N., Lennon,G., Marra,M., Martin,J
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Geisel,G., Jost,S.

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Fal: 314 286 1810
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the TMAGE Consortium (infosimage llnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 456.
Location/Qualifiers
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Contact: Wilson RK
Washington University School of Medicine
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                       594
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/mol_type="mRNA"
/db_xref="GDB:6040024"
/db_xref="taxon:9606"
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/sex="Female"
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Pred. No. 4.8e-65;
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High quality sequence stop: 370.
Location/Qualifiers
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Fax: 314 286 1810
Email: est@watson.wustl.edu
This Clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S. Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Watterston, R. and Wilson, R. Washu-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
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zt26e06.rl Soares ovary tumor NDHOT Homo sapiens
IMAGE:714274 5', mRNA sequence.
AA293138
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                              GGCCACAGAGTCATCTGCCCAGCTCCTCTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGG 467
                                             CTTGGCCAGTCCAGGGTGGGGGGGCGAAACTCCATAAAGAACCAGAGGGTCTGGGCCCC
                                                                                   (bases 1 to 425)
                             CTTGGCCAGTCCAGGGTGGGGGGGGCGAAACTCCATAAAGAACCAGAGGGTCT-GGCCCC
                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="GDB:5934790"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue_type="ovarian tumor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="IMAGE:714274"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
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                                                                                                                                                                                                                                                                    44.48;
                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                    Score 403; DB 1; Length 425; Pred. No. 4.6e-56;
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AA399124/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 402)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost Hillier,L., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-Marck EST Project 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA399124 402 bp mRNA linear EST 16-8 zt49a02.rl Soares ovary tumor NDHOT Homo sapiens cDNA clone IMAGE:725642 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
Contact: Wilson RK
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                                               Conservative
                                                                                                                   double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. "
                                                                                                                                                                                               /tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                      /db_xref="GDB:5937549"
/db_xref="taxon:9606"
/clone="IMAGE:725642"
                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                          'sex="Female"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                            40.7%;
99.3%;
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                                          Score 369; DB 1; Le
Pred. No. 1.6e-50;
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AA481356
                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
This clone is available royally-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 219.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-Merck EST Project 1997
Unpublished (1997)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
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clone="IMAGE:756485"
|sex="Female"
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/mol_type="mRNA"
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                                                                                                                                                                 Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 547)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                          5', mRNA sequence.
BM854082
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K-EST0136380 S22SNU16n1 Homo
5', mRNA semience
                                                                                                            Email: yongsung@mail.kribb.re.kr
Plate: 145 row: D column: 09
High quality sequence stop: 547.
Location/Qualifiers
                                                                                                                                                                                                                                                      21C Frontier Korean EST Project 2001
Unpublished (2002)
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                                                                                                                                                                                                                                           Contact: Kim YS
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                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
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                                                     /organism="Homo sapiens"
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/db_xref="taxon:9606"
/tissue_type="Ascites"
/cell_type="Lymphoblast-like"
                         gex="F"
                                         'clone="S22SNU16n1-145-D09"
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98.9%;
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Pred. No. 1.8e-46;
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RESULT 11
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Matches 335; Conser
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1 (bases 1 to 511)

Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOllveira, P.S., Bucher, P., Jongeneel, C.V., Brunstein, A., Geoliveira, P.S., Bucher, P., Jongeneel, C.V., and C. Harre, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and C. Marce, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J.
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PM1-NN1207-211200-013-d11 NN1207
                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                             sequence tags
                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF
                                                                                                                                                                                                                                                                        Simpson, A.J.
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                                               Brazil
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/clone lib="S22SNU16n1"
/note="Organ: Stomach; Vector: pT773-Pac; Site 1: EcoRI;
/note="Torgan: Stomach; Vector: pT773-Pac; Site 1: EcoRI;
/note="Torgan: S22SNU16 library was contributed by the
Soares laboratory and it was constructed as described by
Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. RNA was prepared from harvested
cells of SNU-16 culture. SNU-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park J.G. et al.
(1990), Cancer Res 50: 2773-2780."
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/lab_host="DH10B"
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99.7%;
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Pred. No. 6.3e-45;
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밁 S 밁 Ś 밁 S 밁 Ś 문 ঠ 밁

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AUTHORS
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High quality sequence stop: 511.
Location/Qualifiers
                                                                                Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 511)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,

O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGAC
                                 Simpson, A.J. Shotgun sequencing of the human transcriptome with ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1&t2=PM1-NN1207-
211200-013-d11&t3=2000-12-21&t4=1)
                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PM1-NN1207-050401-013-d11
                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN1207"
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99.1%;
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Pred. No. 1.3e-40;
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RESULT 13
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 308)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGAC
                                                           Homo sapiens
                                                                           Homo sapiens (human)
                                                                                                                   CN277578.1 GI:47293992
                                                                                                                                     17000600180739 GRN_PRENEU
CN277578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM1&t2=PM1-NN1207-050401-013-d11&t3=2001-04-05&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10737800
Contact: Simpson A.J.G.
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Email: asimpson@ludwig.org.br
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: +55-11-2704922
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Location/Qualifiers
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/mol type="mRNA"
/db xref="taxon:9606"
/dev stage="Adult"
/clone lib="NN1207"
/clone lib="NN1207"
/clone="Torgan: nervous normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-Tibrary was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application NO. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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99.1%;
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Pred. No. 1.3e-40;
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sapiens cDNA 5', mR
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Contact: Brandenberger R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Pax: 650 473 7760
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 363)

Ansorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S. EST (Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.)

Unpublished (1999)
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                                                                                                                                                   AL133867 363 bp mkb DKFZp761H1914 r1 761 (synonym: hamy2) DKFZp761H1914 5', mRNA sequence.
AL133867 GI:6602054
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Length: 308 Std Error: 0.00
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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99.4%;
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Pred. No. 5.1e-40;
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RESULT 15
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                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 319)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Ragai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jongeneel,C.V., Briones,M.T., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone (DKFZp761H1914) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heidelberg/Germany) within the cDNA sequencing consortium German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: MIPS
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BF903767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No s1 sequence available.
                                       Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                               BF903767.1 GI:12295226
                                                                                                                                                                                                                                                                                                                                                                                                 BF903767
proc. Natl. A
                                                              Simpson, A.J.
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/dev stage="adult"
/lab_host="DH10B"
/lab_host="761 (synonym: hamy2)"
/note="Vector: pSport1; Site_1: Not1; Site_2:
/note="Vector: pSport1; Site_1
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Acad. Sci. U.S.A.
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. MT0198 Homo sapiens cDNA,
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(7),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM1&t2=PM1-MT0198-
191200-007-d11&t3=2000-12-19&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 19
High quality sequence stop: 319.
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Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 29.9%; Score 271.2; DB 2; Length 319;
Similarity 92.8%; Pred. No. 1.5e-34;
95; Conservative 0; Mismatches 21; Indels 2
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                                                                                AGGCTCATTGCCAATTCA
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/mol type="mRNA"
/db_xref="taxon:9606"
/dev stage="Adult"
/clone_lib="MT0198"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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   | AC012370 Homo<br>AC005049 Homo   | AL662871 Human   | AL355870   | AC127088 Homo s<br>AL161916 Human  
   | CR788295 Danio<br>BX119924 Human   | AL662859<br>AC027802   | AC003004<br>BX000360  | AL136091<br>AL357560   | AY587020<br>AL133275   
   | AF361481<br>AY207429  | AB100084 Pan<br>M81890 Human   | AC117374  | AC008737   | AC144988  
  | AC012183 Homo sapi<br>AC144877 Pongo pyg   | AC104335   | AC144876   | AC005632  | AC093117  
  | AC008581   | AC145130<br>AC046170   | AC011676  | AC072033  | AC040970<br>AL161935   | 283826 Huma<br>AC027272 Ho  
  | AC019045<br>AC092350   |
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121 121 181 181 241 241	Unknown.  Unclassified.  1 (bases 1 to 907)  Minterbottom, J.M., Shimp, L., Boyce, T.M. Implant, method of making same and use treatment of bone defects  Patent: US 6478825-A 398 12-NOV-2002; Location/Qualifiers  1 .907  /organism="unknown" /mol_type="genomic DNA"  /mol_type="genomic DNA"  100.0%; Score 907; DB 6  10 Similarity 100.0%; Pred. No. 1e-24/ 907; Conservative 0; Mismatches  1 GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCU	RESULT 1 AR252642 DEFINITION Sequence 398 from patent US 6478825. ACCESSION AR252642 VERSION AR252642	1480 203.6 22.4 173271 2 AC141623 1481 203.6 22.4 173817 2 AC012141 1482 203.6 22.4 173912 2 AC141075 1483 203.6 22.4 174028 2 AC141075 1484 203.6 22.4 174028 2 AC136441 1485 203.6 22.4 174539 9 AC103558 1486 203.6 22.4 175053 2 AC023226 1488 203.6 22.4 175069 2 AC138897 1489 203.6 22.4 175785 2 AC138897 1489 203.6 22.4 175786 9 AC105339 1491 203.6 22.4 175786 9 AC105339 1492 203.6 22.4 176630 2 AC010684 1491 203.6 22.4 176731 9 AD000751 1492 203.6 22.4 176927 2 AC127469 1494 203.6 22.4 176791 9 AL557140 1494 203.6 22.4 176710 9 AC1557140 1495 203.6 22.4 179048 9 AC014677 1496 203.6 22.4 183573 9 AC09642 1499 203.6 22.4 183523 9 AC073230 1499 203.6 22.4 183523 9 AC073230 1499 203.6 22.4 183573 9 AC090442 1499 203.6 22.4 183573 9 AC090442 1499 203.6 22.4 183523 9 AC073230 1499 203.6 22.4 183573 9 AC090471
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. Match 100.0%; Score 907; DB 6; Length 907; Local Similarity 100.0%; Pred. No. 1e-244; Local Similarity 100.0%; Pred. No. 1e-244; les 907; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	Patent: WO 0193983-A 97 1 Genentech Inc. (US) Location/Qualifi 1907	.di,J.C., Gurney,A.L., nd,W.I. nbrane polypeptides an	Eukaryota; Metazoa; Chordata; Craniata; Mammalia; Eutheria; Primates; Catarrhir 1 Baker,K.P., Desnoyers,L., Gerritsen,M.E		AX358844 907 bp DNA linear PAT 13-FEB-2002 Sequence 97 from Patent WO0193983.	901 TCACACA 907	- Z	841 TGCGGTGAGCCGAGATCGCGCCCTGATTCCAGCCTGGGCGACAAGAGTGAGACTCCATC 900	781 TAGTCCCAGTTACTCGGGAGGCTGAGGCAGGAAAATCGCTTGAACCCAGGAGGCGGACGT 840		661 TGGGAGGCCGAGGCGGGTGGATCACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACA 720 721 TGGTGAAACCTTGTCTACTAAAAATACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGG 780	TGGGAGGCCGAGGCGGGTGGATCACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACA	601 AGCAATTAAAACTGAGAAATGGGCCGGGCACGGTGGCTCACGCCTGTAATCCCCAGCACTT 660	541 ACCITICITGCICTCAGGACCCCAAAGAGTTICATTGTATCATTTTTTACCACAIT 600 541 ACCITCTTGCTCTCAGGACCCCAAAGAGCTTTCATTGTATCTATTGTATTTTTACCACAIT 600		421 TCTGCCCAGCTCCTCTGCTGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAG 480 481 TAAAACCACAGGCTGGATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCA 540	421 TCTGCCCAGCTCCTCTGCTGCCCAGTGGGAGTGGGACGAGGTGGGGCTTTGTGCCAG 480	61 GGGTGGGGGGCAAACTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCA	301 GCAGGAGGGGGACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCA 360
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Secreted and transmembrane polypeptides and nucleic acids encoding
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AX403511
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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21 (bases 1 to 907)

22 (Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dwd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E., Dwd, P., Eaton, D., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Hee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Sthoenfed, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P.

The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment A Bioinformatics Assessment
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                                              Submitted (01-AUG-2003) Department of Bioinformatics, Inc., 1 DNA Way, South San Francisco, CA 94080, USA Location/Qualifiers
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Clark, H.F.
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/organism="Homo sapiens"
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     TAGTCCCAGTTACTCGGGAGGCTGAGGCAGGAAAATCGCTTGAACCCAGGAGGCGGACGT
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1. .907
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/note="PRO1187"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CE 2 (bases 1 to 101777)

CE 2 (bases 1 to 101777)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Campopiano, A., Chang, J., Chazaro, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Devarellano, K., Diaz, J.S., Dodge, S., Faro, S., Choepel, Y., Colangelo, M., Collins, J., Gardyna, S., Faro, S., Ferreira, P., Fizzhugh, W., Gage, D., Galagan, J., Gardyna, S., Faro, S., Ferreira, P., Fizzhugh, W., Graham, L., Grand-Pierre, N., Jones, C., Kagetas, A., Kells, C., Lancoque, K., Jones, C., Karatas, A., Kells, C., Laracque, K., Jones, C., Karatas, A., Kells, C., Levine, R., Liu, G., MacCarthy, M., McEwan, P., McKerran, K., McPheeters, R., Melatim, J., McCarthy, M., McEwan, P., McKerran, K., McPheeters, R., Melatim, J., McCarthy, M., McEwan, P., McKerran, K., McPheeters, R., Melatim, J., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Nell, D., Oliver, J., Reteran, K., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Seanan, S., Severy, P., Spencer, B., Stange-Thomann, M., Stojanovic, N., Senanan, S., Severy, P., Spencer, B., Stange-Thomann, M., Stojanovic, N., Viell, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Jirect Submission
Direct Submission

M., Subrather, A., and Zody, M.
        CE 3 (bases 1 to 10177)

CE 3 (bases 1 to 10177)

RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,

RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,

Bourson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,

Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,

Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,

Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,

Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,

Collymore, A., Cooke, P., Corum, B., DeArellano, K.,

Perreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S.,

Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Hagos, B.,

Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,

Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,

Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,

Macdonald, P., Major, J., Manning, J., Matthews, C., McCatthy, M.,

Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,

Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,

O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,

Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,

Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,

Vasailley, H., Venkarraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,

Vasailley, H., Venkarraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,

Vasailley, H., Venkarraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,

Vasailley, H., Wu, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        901
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Homo sapiens chromosome 8, clone RPI1-118P12, complete sequence.
ACLUSZIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (26-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 101777) ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Viel, R.,
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Direct Submission
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AL Submisted (06-FBB-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 10177)
Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
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Anderson, S., Cook, A., Cooke, P., Corum, B., Darellano, K.,
Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
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Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
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Meldrim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J.,
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Nguyen, C., Nicoll, R., Nobbu, C., O'Connor, T., O'Donnell, P.,
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Nguyen, C., Nicoll, R., Nobbu, C., Metta, R., Rise, C., Regov, P.,
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Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
Vassiliev, H., Venkataman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
N., Manda, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
N., A., F.A. & Green, P. (1996-1997)
N., A., F.A. & Green, P. (1996-1997)
N., A., Manda, M., Manda, M., M., M.
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Only the middle 101.8 kilobases of this clone are being submitted. The remainder overlaps either accession number AC067930 [WICGR project L10100] or accession number AC105219 [WICGR project L23081].

/rpt\_family="(CCCCCA)n" 3950. .4302 /db\_xref="taxon:9606" /chromosome="8" organism="Homo sapiens Location/Qualifiers clone="RP11-118P12" \_family="MSTA" \_family="G-rich" \_family="GC\_rich" \_family="GC\_rich" type="genomic DNA" family="MLT1D-int" family="MLT1D" family="MLT1B" . 8900 .6583

Query Match 100.0%; Score 907; DB 9; Length 101777; Best Local Similarity 100.0%; Pred. No. 1.1e-244; Matches 907; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	repeat_region 38778 . 38486 (-A)n" /rpt_family="(CA)n"	38211	repeat_region 38154	repeat_region 3800038153	repeat_region complement(34498.34792) /rpt family="AluSq"	family="	repeat_region 3181631845 /rot family="(TA)n"	repeat_region 292642321		28604	/rpt_tamily="GC_rich" on 2856928599	28554	ile clone coverage"	.28593	="<30 qual 28500	.28386	.28388 .28388	628365	amily="Alu .28094	-		repeat_region complement (2551925676)	repeat_region complement(2309623135)	family="MER53 721518	/rpt	region	rpt family="AluSx" region 1823318299	region	/rpt _region 17717	region 17644	_ /rpt_fam _region 16927	region 15716	repeat region 15399. 15698
RP11-661A12,	ACO67930 174906 bp DNA linear PRI		Db 17953 TCACACA 17947	Qy 901 TCACACA 907	Db 18013 TGCGGTGAGCCGAGATCGCGCCGCTGATTCCAGCCTGGGCGACAAGAGTGAGACTCCATC 17954	QY 841 TGCGGTGAGCCGAGATCGCGCCGCTGATTCCCAGCCTGGGCGACAAGAGTGAGACTCCATC 900	Db 18073 TAGTCCCAGTTACTCGGGAGGCTGAGGCAGGAAAATCGCTTGAACCCCAGGAGGCGGACGT 18014	QY 781 TAGTCCCAGTTACTCGGGAGGCTGAGGCAGGAAAATCGCTTGAACCCCAGGAGGCGGACGT 840	Db 18133 TGGTGAAAACCTTGTCTAACTAAAAATACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGG 18074	Qy 721 TGGTGAAACCTTGTCTACTAAAAATAAATTAGCCAGGCACAGTGGTGTGCACTGG 780	Db 18193 TGGGAGGCCGAGGCGGTGGATCACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACA 18134	Qy 661 TGGGAGGCCGAGGCGGGTGGATCACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACA 720	Db 18253 AGCAATTAAAACTGAGAAATGGGCCGGGGCACGGTGGCTCACGCCTGTAATCCCAGGACTT 18194	Qy 601 AGCAATTAAAACTGAGAAATGGGCCGGGCACGGTGGCTCACGCCTGTAATCCCCAGCACTT 660	Db 18313 ACCTTCTCAGGACCCCAAAGAGCTTTCATTGTATCTATTGATTTTTACCACATT 18254	QY 541 ACCTTCTTGCTCTCAGGACCCCAAAGAGCTTTCATTGTATCTATTGATTTTTACCACATT 600	Db 18373 TAAAACCACAGGCTGGATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCA 18314	Qy 481 TAAAACCACAGGCTGGATTTGCCTGCGGGCCATGGTCCTGTCTAGGGCAGCAATTCTCA 540	Db 18433 TCTGCCCAGCTCCTCTGCTGCTGGCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAG 18374	Qy 421 TCTGCCCAGCTCCTCTGCTGCTGGCCAGTGGGAGTGGCAGGGGGGGG	Db 18493 GGGTGGGGGCAAACTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCA 18434	QY 361 GGGTGGGGGGCAAACTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCA 420	Db 18553 GCAGGAGGGGGACAGTTCTGTTGTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCA 18494	Qy 301 GCAGGAGGGGGACAGTTCTGTTGTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCA 360	18613 GAGAGGACACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACA	241	18673 GAGAGAGTGTCCTGGGTCAGGGACGCAGAGGGCCCTCTGGTTACC	181 GAGAGAGTGTCCTGGGTCAGGGACGCAGAGACGCCCCACAGACTCCAGCCCCTTTGTTACC	18733 ATGCTACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCTTGCC	Qy 121 ATGCTACCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCTCCTTGCC 180	18793 CCCTAGGGGTCTGGATTTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGA	61 CCCTAGGGGTCTGGATTTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCCATAGGGGA	Db 18853 GGACTCTGAAAGGTCCCAAGGAGCTGCTGAGCCCCCAAGGAAGTGGTTCCAACCTTGGAC 18794

REFERENCE AUTHORS

JOURNAL

REFERENCE AUTHORS TITLE

ORGANISM

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COLLYMOTE, A., COOKE, F., DEARELLAND, N., DEWEL, N., DEGGE, D., DOGGE, S., DOMING, M., DOYLE, M., FETTELER, P., FILTHUGH, W., GGG, D., DOGGE, S., JONGE, S., GOYELTE, M., GRAMM, M., GGG, D., DOGGE, S., JERCH, M., GRAMM, M., GRAMM, M., GRAMM, M., CRAMM, M., CARLES, A., HARDE, M., LARGOR, M., LARGOR, R., JONGE, T., MARCHAN, M., CARLES, A., LARGOR, M., LARGOR, R., JONGE, T., MARCHAN, M., LARGOR, M., LARGOR, R., JONGE, T., MARCHAN, M., LARGOR, M., LARGOR, R., MARCHAN, M., MERCHAN, M., LARGOR, R., MARCHAN, M., MERCHAN, M., ME
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dewar,
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1 (bases 1 to 174906)

Birren,B., Nusbaum,C. and Lander,B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
----- Project Information
Center project name: L10100
Center clone name: 661_A_12
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/db_xref="taxon:9606"
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                                                                         GAGAGAGTGTCCTGGGTCAGGGACGCAGAGGGCCTCACAGACTCCAGCCCCTTTGTTACC
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complement (38896. .38903)
/note="a30 qual SNGL region"
complement (38898. .38902)
/note="probably ACTGA"
complement (38984. .39281)
/rpt_family="AluSx"
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complement(71849...
/rpt_family="Alusx"
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complement(38880. .38983)
/rpt_family="MSTC"</pre>
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71273. .71458
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41752. .41933
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/rpt family="MSTC"
complement (39366. .39668)
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/note="<30 qual SNGL region"
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/note="probably ACTGGTGGC"
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complement(38859.
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/rpt_family="(CGGGG)n"
37077. .37162
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2 (bases 1 to 207636)
Waterston,R.H.
Direct Submission
Submitted (30-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Jun 7, 2000 this sequence version replaced gi:7109639.
                                                                                                                                                                                                                             AC019122
AC019123 GI:8318560
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                           ACU19122
207636 bp
Homo sapiens chromosome 8 clone
SEQUENCE, 12 unordered pieces.
ACC10177
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 207636)
Waterston, R. H.
                                                                                                                        The sequence of Homo sapiens clone 
Unpublished
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RP11-545C16, WORKING
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Sequencing vector: M13; 88*
Sequencing vector: plasmid; 12*
Chemistry: Dye-primer ET; 88* of reads
Chemistry: Dye-terminator B1g Dye; 12* of reads
Chemistry: Dye-terminator B1g Dye; 12* of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 198432 bases at least Q40
Consensus quality: 201424 bases at least Q30
Consensus quality: 203070 bases at least Q20
Insert size: 206536; sum-of-contigs
Quality coverage: 6.36 in Q20 bases; sum-of-contigs
Quality coverage: 5.66 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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11013
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3688
  78482. .106509 // note="assembly_name:Contig22" 106610. .130451
                                           /note="assembly_name:Contig21"
78482. .106509
                                                                                              /note="assembly_name:Contig20"
54332. .78381
                                                                                                                                            /note="assembly_name:Contig19"
35140. .54231
                                                                                                                                                                                             /note="assembly_name:Contig18"
23840. .35039
                                                                                                                                                                                                                                                                                                                                                            /note="assembly_name:Contig15"
                                                                                                                                                                                                                                              /note="assembly_name:Contig17"
16641. .23739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/chromosome="8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                note="assembly_name:Contig16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (28-JAN-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 16, 2001 this sequence version replaced gi:12584321. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Travers, M., Travis, N., Trigilio, Wilson, B., Wu, X., Wyman, D., Ye, W Zembek, L., Zimmer, A. and Zody, M.
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1 (bases 1 to 164959)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 8, clone RP11-545C16
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Homo sapiens chromosome 8 clone RP11-545C16 map
IN PROGRESS ***, 70 unordered pieces.
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                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 70 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: L11736
Center clone name: 545_C_16
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Bandman,O., Lal,P., Hillman,J.L., Yue,H., Reddy,R., Guegler,K and Baughn,M.R.
Composition for the detection of genes encoding receptors and proteins associated with cell proliferation
Patent: US 6183968-A 73 06-FEB-2001;
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Guegler, K.J

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                                                                                                                                    Patent: WO 0192581-A 5524 06-DEC-2001;
CORIXA CORPORATION (US)
Location/Qualifiers
                                                                                                                                                                                         Algate, P.A., Harlocker, S.L. and Jones, R. Compositions and methods for the therapy
                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Sequence 3167 from Patent
CQ460389
CQ460389.1 GI:41426008
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                                                                                                                               Conservative
                                                                                                                                                                                        /organism="Homo sapiens"
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                                                                                                                                        44.48;
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Pred. No. 1.6e-102;
0; Mismatches 0;
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                                                                 GCGGCAAACTCCATAAAGAACCAGAGGGTCT-GGCCCCGGCCACAGAGTCATCTGCCCAG
                                                                             GCGGCAAACTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCCAG 429
                                                                                                            GGACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGG
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 AGGCTGGATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTG
                                CTCCTCTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGTAAAACCAC 489
                     CTCCTCTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGTAAAACCAC
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CORPORATION (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="unassigned DNA"
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Pred. No. 6.4e-93;
0; Mismatches 0; Indels
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Sequence 6113 from Pate
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CQ463335.1 GI:41428954
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Patent: WO 0192581-A 6113 06-DEC-2001;
CORIXA CORPORATION (US)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No. 6.4e-86;
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Homo sapiens (human)

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Search completed: September 15, 2005, 17:07:39 Job time : 4546 secs
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Matches 224; Conservative
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Patent: WO 0102568-A 2068 11-JAN-2001;
CHIRON CORPORATION (US); HYSEQ, INC. (US)
Location/Qualifiers
1. 399
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                   /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No. 1.2e-51;
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Sequence 152, App Sequence 152, App Sequence 38633, A Sequence 38633, A Sequence 11534, Sequence 11534, Sequence 119, App Sequence 119, App	Sequence 574, A Sequence 11, A Sequence 88, A Sequence 294231 Sequence 29423	Sequence 399, A Sequence 788, A Sequence 58, Ap	Sequence 3, Appli Sequence 3, Appli Sequence 399, Appl	Sequence 1, Appl Sequence 77, Appl Sequence 61, Appl	Sequence 5, Appli Sequence 5700, Ap	Sequence 5, Appli	Sequence 1714, Ap	Sequence 132, App Sequence 1579, Ap	Sequence	Sequence 218458,	Sequence 218458,	Sequence 99, Appr Sequence 790, Appr Sequence 218457.	Sequence 1456, Ap Sequence 232, App	57	24		Ď-	σ.	5.	æ -	quence 32, equence 32	4,	ence 30	ence	ence	ence	ence	ence	ence	ence	2 2
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Membrane-bound protein PRO1187 encoding cDNA.
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Human PRO1187 (UNQ601) nucleotide sequence
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                                                                       ACA68022 standard; cDNA; Novel human secreted and US2002177164-A1.
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Novel human secreted and transmembrane
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ACA88471 standard; cDNA; 907 BP.
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Human cDNA encoding secreted/transmembrane
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Human PRO1187 cDNA.
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     ABT44557 standard;
Human PRO1187 cDNA
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Human cDNA encoding secreted/transmembrane
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RESULT 26
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RESULT 31
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Human membrane bour
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US2003054403-A1.
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                                                                                   ADC78044 standard; cDNA; Novel human secreted and US2003096972-A1.
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13-FEB-2003.
                                                                     Human PRO polynucleotide US2003100712-A1.
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Novel human secreted and
US2003045687-A1.
06-MAR-2003.
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31-OCT-2002.
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Human PRO polynucleotide
US2003100728-A1.
29-MAY-2003.
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ADD75790 standard; cD
Novel human secreted
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Novel human secreted and
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Novel human secreted and
US2003096362-Al.
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Best Local Similarity
RESULT 116
ID ADD773814 standard; cl
DE Human PRO polynucleot
PN US2003100710-A1.
PD 29-MAY-2003.
                 RESULT 119
ID ADD857
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Human PRO polynucleotide
US2003100710-A1.
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Novel human secreted and
US2003100730-A1.
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Novel human secreted and
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Novel human secreted and
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                                                       ADD85774 standard; cDNA; 907
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16-OCT-2003.
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US2003100723-A1.
                                          ADF94563 standard; cDNA;
Novel human secreted and
US2003096964-A1.
22-MAY-2003.
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22-MAY-2003.
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22-MAY-2003.
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RESULT 131
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RESULT 137
ID ADI29818 standard; c
DE Novel human secreted
PN US200396961-A1.
PD 22-MAY-2003.
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Best Local Similarity
RESULT 134

ID ADG34093 standard; c
DE Novel human secreted
PN US2004006206-A1.
PD 08-JAN-2004.
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RESULT 133
ID ADH20177
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ADM27215 standard;
Novel human secreto
US2004044179-A1.
                                                                                ADI29818 standard; cDNA; Novel human secreted and US2003096961-A1.
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Novel human secreted and
US2004006206-A1.
08-JAN-2004.
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27-NOV-2003.
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Novel human secreted and
US2003096965-A1.
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RESULT 147
ID ABL8018° -
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Best Local Similarity
RESULT 139
ID ADK66573 standard; c
DE Human PRO polynucleo
PN US2004044180-A1.
PD 04-MAR-2004.
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RESULT 144
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RESULT 141
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                                                                                         ABL82546 standard; cDNA; 480 Human ovarian cancer related
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Novel human arginine-rich
US2004053250-A1.
18-MAR-2004.
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Connective tissue related gen
US2003054375-Al.
20-MAR-2003.
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(GETH ) GENENTECH INC.
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   ABL80189 standard; cDNA; 425 Human ovarian cancer related
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Human PRO polynucleotide
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Human polynucleotide SEQ ID NO
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ry Match 100.0%;
t Local Similarity 100.0%;
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(XUEA/) XUE A.
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No. 8.3e-250;
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cDNA clone

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(CORI-) CORIXA CORP.
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Human digestive system &
WO200155314-A2.
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WO200192581-A2.
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WO200102568-A2.
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(CORI-) CORIXA CORP.
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(CORI-) CORIXA CORP.
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Human ovarian cancer related
                                                       Human cardiovascular system US2003059908-Al.
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 ADJ08002 standard;
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(HYSE-) HYSEQ INC.
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Human cardiovascular system ar
WO200155321-A2.
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Human cardiovascular system ar
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Human cardiovascular system associated polypeptide-related DNA SeqID1943.
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ADE47138 standard; DNA; 19345
Human cardiovascular system re
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No. 5.7e-50;
                                                                                                          212.2; DB 13;
No. 5.9e-50;
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8 4.
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5.9e-50;
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Best Loc
RESULT 170
ID AAK91'
DE Hum'
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RESULT 166
ID ADJOCCO
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RESULT 171
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10-JUN-2004.
(ISIS-) ISIS PHARM INC.
(ISIS-) 1SIS PHARM INC.
23.4%; 8
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Human cardiovascular system associated polypeptide-related
US2004005575-A1.
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27-MAR-2003.
                                                                   Human liver-related US2003077602-A1.
                                                                                          ADJ15405 standard;
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11-APR-2002.
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(HUMA-) HUMAN GENOME SCI INC
23-3%;
ry Match 23-3%;
83-8%;
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12-SEP-2003.
(SAGR.) SAGRES DISCOVERY.
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ry Match 23.3%;
t Local Similarity 83.8%;
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ry Match 23.4%;
t Local Similarity 73.6%;
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C
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ch 23.3%;
l Similarity 83.8%;
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DNA; 126990 BP
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d genomic DN
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No.
                     211.2; DB 1
No. 1.3e-49;
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No. 1.3e-49;
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No. 1.3e-49;
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No. 1.3e-49;
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No. 1.8e-49;
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No. 1.8e-49;
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RESULT 182
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RESULT 181
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  ABX59843 standard; cDNA; 19616 BP. cDNA encoding novel human musculoskeletal system antigen #2187.
                                                                                         ABA16094 standard; DNA; 19616
Human nervous system related p
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Human musculoskeletal system related polynucleotide
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                                                                                        Human nervous system
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ry Match 23.1%;
t Local Similarity 86.7%;
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23.1%;
ry Match 23.1%;
t Local Similarity 85.1%;
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ry Match 23.1%;
Local Similarity 82.6%;
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1.4e-49;
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US2002147140-A1

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Query Match
Best Local Similarity
RESULT 183
ID ADJ30593 standard; D
DE Human musculoskeleta
PN US2004009488-A1.
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RESULT 185
ID AAL06745 standard;
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02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
23.1%;
ery Match 23.1%;
                                                                                                                              Human immune/haematopoietic antigen WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                    AAI62649 standard; DNA; 691 BP. Human breast or ovarian antigen
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                                                       AAL06744 standard; DNA; 16225 BP. Human reproductive system related WO200155320-A2.
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Human breast or ovarian antigen genomic
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Human reproductive system related
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(HUMA-) HUMAN GENOME
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Human musculoskeletal system-associated
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(HUMA-) HUMAN GENOME
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(HUMA-) HUMAN GENOME
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system related antigen DNA
DNA; 16225
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No.
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No. 3.8e-49;
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No. 3.8e-49;
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No.
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No. 1.1e-49;
                  209.2;
No. 4e-
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No.
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4e-49;
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Human novel lung re
US2003054368-A1.
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                                                         ABK83459 standard; cDNA; 128978
Human cDNA differentially expres
                                                                                                                       Human kinase genomic US2004175751-A1.
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Human serine/threonine kinase
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ry Match 23.1%;
t Local Similarity 83.3%;
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                                                   WO200228999-A2.
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US2003166215-A1.
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                                 (GENE-)
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79.7%;
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DNA; 128978 BP
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82.5%;
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No. 6.6
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No. 6.6e-49;
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No.
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No.
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No. 6.6e-49
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4e-49;
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6 ?
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                                                             granulocytic
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.2e-49;
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.6e-49;
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.2e-49;
                DB
-49;
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12-L
(EXEL-)
Query Match
Best Local 9
RESULT 201
ID ADR529'
DE Drug
PN WO2'
PD 26
PA '
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Best Local S:
RESULT 204
ID ADQ97727 6
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02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
23.0%;
21Y Match 23.0%;
31Y Match 23.6%;
                                                                                                                                                                                                                                                                                                                                                                   Genomic sequence #811 encoding novel human WO20015343-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                   ADQ97727 standard; DNA; 73063 BP.

Human cancer associated sequence HD10-034,

W02004060304-A2.

22-JUL-2004.

22-JUL-2004.

(SAGR-) SAGRES DISCOVERY INC.

SAGR-) SAGRES DISCOVERY INC.

23.0%; Score 208.8;

STY Match

23.0%; Pred. No. 9.4%
ADN06353 standard;
Human FLAP genomic
WO2004035741-A2.
                                                                                                    AAK79905 standard; DNA; 2744 BP. Human immune/haematopoietic anti
                                                                                                                                                                         WO2003080808-A2.
02-OCT-2003.
                                                                                                                                                                                                                                                                               Connective tissue US2003054375-A1.
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(PROT-) PROTEIN DESIGN LABS INC.

EXY MATCH
23.0%; Score
23.7%; Pred.
                                                                                                                                                                                                           ADE82948 standard;
                                                                                                                                                                                                                                                                                                       ADB61068 standard;
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Human soft tissue
WO2004048938-A2.
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                                                                     (HUMA-) HUMAN GENOME
                                                                                         WO200157182-A2.
                                                                                                                                     (SAGR-) SAGRES DISCOVERY.
ry Match 23.0%;
t Local Similarity 84.6%;
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ry Match 23.0%;
Local Similarity 83.6%;
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TWINE N.
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                                                                                                                                                                                                                                                                                         related genomic DNA
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sarcoma-upregulated
                                            SCI INC.
23.0%;
82.3%;
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23.1%;
79.7%;
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            398800 BP.
SEQ ID NO:1
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No. 9e-49;
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No. 9.4e-49;
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No. 9.6e-49;
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                                            .2; DB
4e-49;
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1.6e-49;
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7.7e-49;
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.5e-48;
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Best Local Similarity
RESULT 213
ID ADD65796 standard; D
BHuman 16p133 sequenc
PN W02003072827-A1.
PD 04-SEP-2003-A1
PA (CHIL-) CHILDREN'S H
                                           Best Local Similarity RESULT 218
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Best Local Similarity
RESULT 216
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RESULT 212
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RESULT 210
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Human sulphate transporter protein WO200259306-A2. 01-AUG-2002.
                                                                                                   Human sulphate transporter WO200181412-A2.
                                                                                                                                                                                                                                                                                                                                                                         AAK71190 standard; DNA; 3139 BP. Human immune/haematopoietic antigen W0200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human 16p133 sequence WO2003072827-A1.
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Human soft tissue sarcoma-upregulated
                                                                                                                                                                                                                                                                                  Human soft tissue sarcoma-upregulated WC2004048938-A2.
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(HUMA-) HUMAN GENOME SCI INC.
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                                  AAL50687 standard; DNA; 31766 BP
                                                                                                                         AAD22781 standard;
                                                                                                                                             (PROT-) PROTEIN DESIGN LABS

xy Match 22.9%;
t Local Similarity 85.0%;
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xy Match 22.9%;
t Local Similarity 85.0%;
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                                                                                                                                                                                                                                                                                                          ADQ20461 standard;
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Thyroid cancer related gene
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ry Match 23.0%;
t Local Similarity 82.3%;
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                                                                            PEKE ) PE CORP NY
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22.9%;
79.2%;
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nsporter protein
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5.4e-49;
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2.5e-48;
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22-JUL-2004.
(SAGR-) SAGRES DISCOVERY INC.
(SAGR-) SAGRES DISCOVERY INC.
22-8%;
21Y Match 24-milarity 82.0%;
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Human cDNA differentially express;
WO200228999-A2.
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Human MORF carcinoma associated g
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WO2004060304-A2.
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Human nervous system related
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                                                     Human Morf genomic
                                                             ADC85236 standard;
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                                                                                    (SAGR-) SAGRES DISCOVERY.

CY Match 22.8%;
Local Similarity 84.0%;
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h 22.8%;
similarity 84.0%;
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22.8%;
arity 84.0%;
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e 207.2; DB 10;
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No.
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09-AUG-2001.

(HUMA-) HUMAN GENOME SCI INC.

22.7%;

ery Match 22.7%;

82.2%;
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                                                                                                                ABZ68089 standard; DNA; 16146 BP. Human secreted protein encoding g W0200277186-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADA44551 standard; DNA; 16146 E
Human secreted protein DNA SEQ
WO2003000865-A2.
                                                                                                                                                                                              ABT17011 standard; DNA; 16146 I
Human secreted protein-related
WO200277188-A2.
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                                             ACN44482 standard; DNA; 34096 BP.
Human genomic sequence hCG26017.
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16-AUG-2001.
(HUMAN) HUMAN GENOME SCI INC.
                                                                                                              Human immune/haematopoietic antigen W0200157182-A2.
                                  AAK81748 standard; DNA; 451 Human immune/haematopoietic
                                                                                                                                                                                                             Human nervous system related WO200159063-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cancer associated sequence HD08-008,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABN87883 standard;
Human glutathione
WO200242320-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               жымву533 standard; DNA; 48436 BP.
Human corneal N-acetylglucosamine-6-sulfotransferase
US2002061562-A1.
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01-FEB-2001.
                            WO200157182-A2.
                                                                       (HUMA-) HUMAN GENOME SCI INC.
ry Match 22.7%;
t Local Similarity 84.9%;
                                                                                                           09-AUG-2001
                                                                                                                                                                                                                                    ABA20765 standard;
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ry Match 22.7%; Score 206.2; DB 5;
t Local Similarity 84.7%; Pred. No. 4.1e-48;
                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
ry Match 22.7%;
Local Similarity 84.9%;
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ry Match 22.7%;
Local Similarity 79.0%;
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ry Match 22.7%;
Local Similarity 84.7%;
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CY Match 22.7%; Score

Local Similarity 81.7%; Pred.
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       HUMAN GENOME SCI INC
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84.9%;
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84.4%;
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79.9%;
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(GSR)
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Pred. No. 4.5e-48;
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No.
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No. 5.
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No. 5
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No.
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No. 6.4e-48;
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No.
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5.2e-48;
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9.7e-49;
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7.2e-48;
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.5e-48;
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AGR-) SAGRES DISCULT 255

ID ABX16034 stand-
DE Human gene
PN US20021

PD 03-7

PA 03-7
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RESULT 251
ID ACMARCA
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Best Local Similarity
RESULT 247
ID ABA16121 standard; D
B Human nervous system
PN W0200159063-A2.
PD 16-AUG-2001.
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RESULT 250
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Best Local Similarity
RESULT 248
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                                                                                                        WO2003039484-A2.
                                                                                                                 ADE95944 standard; DNA; 59554 BP.
Human TK2 gene genomic DNA sequence.
                                                                                                                                                                                      Human TK2 gene.
WO2003008583-A2.
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                                                                                                                                                                                                           ADB72434 standard;
                                                                                                                                                                                                                                                                                Human TK2 carcinoma associated
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ry Match 22.7%; Score
t Local Similarity 83.6%; Pred.
                                                                                    (SAGR-) SAGRES DISCOVERY.
                                                                                                                                             (SAGR-) SAGRES DISCOVERY.
ry Match 22.7%;
t Local Similarity 86.3%;
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ry Match 22.7%;
t Local Similarity 83.6%;
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                                             DNA;
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cium channel transporter
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6.3e-48;
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6.3e-48;
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2.8e-48;
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2.8e-48;
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9.7e-49;
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Best Loca
RESULT 258
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Best Local S
RESULT 261
RESULT 264
ID AAK859
DE Human
PN WO2001
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ID AAK859
DE Human
PN WO2001
PD 09-AUG
PA (HUMA-
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RESULT 260
ID ABQ726
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Best Local Similarity
RESULT 256
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O9-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
22.6%;
ery Match 22.6%;
ery Match 86.5%;
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09-AUG-2001.

(HUMA-) HUMAN GENOME SCI INC.

(HUMA-) HUMAN GENOME SCI INC.

22.6%;

ery Match 22.6%;

ery Match 86.5%;
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09-AUG-2001.

(HUMA-) HUMAN GENOME SCI INC.

(HUMA-) HUMAN GENOME SCI INC.

22.6%;

ery Match 22.6%;
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                                                                                                                                                                                          AAK85983 standard; DNA; 48037 BP. Human immune/haematopoietic antigen W0200157182-A2.
                                                                                                                                                                                                                                                                                       AAK84729 standard; DNA; 48037 BP. Human immune/haematopoietic antigen W0200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                   ABQ72698 standard; cDNA; Human MDDT encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding novel WO200157187-A2.
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Human chromodomain helicase DNA binding protein
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                                                                                              AAK84730 standard; DNA; 48045 BP.
Human immune/haematopoietic antigen
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                        (INCY-) INCYTE GENOMICS INC.
ry Match 22.6%;
t Local Similarity 82.6%;
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(HYSE-) HYSEQ INC.
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(HUMA-) HUMAN GENOME SCI INC.
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(DFRA/) DI FRANCESCO
(BEAS/) BEASLEY E M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS23041 standard;
 Human immune/haematopoietic WO200157182-A2.
                       AAK85984 standard;
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system related antigen
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bone marrow polypeptide
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22.7%;
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No. 3.6e-48;
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No. 1e-47;
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No. 1.5e-48;
                                                 205.4; DB 4;
No. 7.6e-48;
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No. 2.5e-48;
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                                                                                                             SEQ
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               IJ
                                                              48045;
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                                                                                                                                                                                                         ID NO:40795
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               NO:40796
                                                                                                              NO:39542
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Query Match
Best Local Similarity
RESULT 265
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PA
                    Best Local Similarity RESULT 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADC85367 standard;
Mouse Blm coding so
WO2003045230-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ01022 standard; DNA; 56520 Wild type PG1 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PG1 genomic co
WO9932644-A2.
                                                                                                                                                                                                                                                        Human carcinoma associated US2004072154-A1. 15-APR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADA02888 standard; DNA; 96594 l
Human BLM carcinoma associated
W02003057146-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1999.
(GEST ) GENSET.
                                                                                                                           (BOST-) BOSTON PROBES INC.
(DAKO-) DAKOCYTOMATION DENMARK AS.
(DAKO-) 22.6%; Score
                                                                                                                                                                     Alu-repeat consensus WO2003027328-A2.
                                                                                                                                                                                                                                                                                                                                                        Human BLM gene.
WO2003008583-A2.
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YY Match
12.6%;
Local Similarity 83.9%;
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ry Match 22.6%;
t Local Similarity 83.9%;
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                                                                                Human BHD mutant truncated
                                                                                                                                                                                         ADH59596 standard; DNA; 301
                                                                                                                                                                                                                                                                                           ADM74483 standard; DNA; 96594
                                                                                                                                                                                                                                                                                                                                                                              ADB72626 standard;
AAL52588 standard; cDNA; 36
Human BHD mutant truncated
                                                                         WO2003102149-A2.
                                                                                             AAL52585 standard; cDNA;
                                                                                                                                                                                                                                    (MORR/) MORRIS D W.
                                                                                                                                                                                                                                                                                                                                               30-JAN-2003
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                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                              DNA;
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22.6%;
86.5%;
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85.8%;
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83.9%;
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78.8%;
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78.8%;
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No. 9.9
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No. 8.
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No.
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No. 7.6
                                205.
No.
                                                                                                                205.2; DB 1
No. 1.2e-48;
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No.
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No. 9.9e-48;
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No. 9.9e-48;
  ID NO:
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                               9.9e-48;
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7.6e-48;
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8.1e-48;
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                                  .2e-48;
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                                          DB 12;
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WO2003102149-A2

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Best Local Similarity
RESULT 276
ID AAL52587 standard; c
DE Human BHD mutant tru
PN W02003102149-A2.
PD 11-DEC-2003.
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RESULT 274
ID AAL52584 standard; of
DE Human BHD coding sec
PN W02003102149-A2.
PD 11-DEC-2003.
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Best Local S
RESULT 281
ID AAK80060
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RESULT :
                             RESULT 282
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Best Local Similarity
RESULT 277
ID AAL52618 standard;
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WO2003102149-A2.
11-DEC-2003.
11-DEC-2003.
(USH) US DEPT HEALTH & HUMAN SERVICES.
(USH) US DEPT HEALTH & HUMAN SERVICES.
R1.2%; Pred. No. 3.2e-48;
                                                                                                                                                                                                                                                                                                                  Human immune/haematopoietic antigen W0200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                    Human BHD mutant truncated cDNA SEQ W02003102149-A2.
11-DEC-2003.
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
STY Match 22.6%; Score 205.2;
The conditional Similarity 81.2%; Pred. No. 3.2
                                                                                                             AAK80060 standard; DNA; 5279 BP.
Human immune/haematopoietic antigen
                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
ry Match 22.6%;
t Local Similarity 83.4%;
                                                                                                                                                                                                                           AAK80062 standard; DNA; 5279 BP.
Human immune/haematopoietic antigen
                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
ry Match 22.6%;
t Local Similarity 83.4%;
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TY Match 22.6%; Score 205.2

L Local Similarity 81.2%; Pred. No. 3
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Human BHD mutant ti
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EXY Match

22.6%; Score 205.2; DB 1

L Local Similarity

81.2%; Pred. No. 3.2e-48;
                                                                      (HUMA-) HUMAN
                                                                                                  WO200157182-A2.
                                                                                                                                                                                                                WO200157182-A2.
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WO2003102149-A2.
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                                          Similarity
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22.6%; Score 205.2
milarity 81.2%; Pred. No. 3
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22.6%; Score 205.2;
milarity 81.2%; Pred. No. 3.2
                                                                       GENOME
  human
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truncated cDNA SEQ
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truncated cDNA SEQ
 DNA; 17131 BP.
an geranylgeranyl
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                                         3 SCI INC
22.6%;
83.4%;
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Pred.
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No. 3.7e-48;
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pyrophosphate
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3.7e-48;
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3.7e-48;
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  (hGGPPS)
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Query
Best Loc.
RESULT 289
ID ABZ97'
DE Hum'
PN W'
PD
Best Loc
RESULT 291
ID ADT
DB
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RESULT 288
ID AAF21311 standard; Dt
DE Human low adenosine &
PN w020062736-A2.
PD 26-0CT-2000.
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Best Local Similarity
RESULT 283
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RESULT 284
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Human nucleic acid (
WO200285308-A2.
31-OCT-2002.
                                                                                                                                                                                                                                                                                                          Human adenosine receptor WO200009525-A2.
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Human nucleic acid
WO200285308-A2.
                                                                     Human pulmonary WO200285309-A2.
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(GEST ) GEN
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YY Match 22.6%;
t Local Similarity 77.8%;
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                                                                                                                            (EPIG-) EPIGENESIS
                                                                                                                                                                                                      (NYCE/) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIG-) EPIGENESIS PHARM INC.
ry Match 22.6%;
t Local Similarity 77.8%;
   ADJ10262 standard; DNA; 51001 BP.
Human geranylgeranyl diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                          ABD20850 standard;
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y 77.8%;
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le antisense
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77.8%;
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77.8%;
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inflammatory
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ceptor related
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inflammatory
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No.
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No. 5.8e-48;
                                                                                                           5.2; DB 10
. 8.1e-48;
                                                                                                                                                                                                                                                                       8.1e-48;
                               8.2
                                                                                                                                                                                    .2; DB 3;
8.1e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .2; DB 3;
7.5e-48;
                                                                                                                                                                                                                                                                                                                                                   .2; DB 11;
7.5e-48;
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7.5e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72
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                               ; DB 11;
.1e-48;
                                                                              DNA #465
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                                                                                                                    DB 10;
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                                                                                                                                                                                                                                                                                                                      NO:63.
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synthase 1

genomic

DNA SeqID

11

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Query
Best Loc.
RESULT 296
ID AAS4)'
DE Gen
PD W'
PD
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RESULT 294
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ID AU
DE HU
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PD 08
PD 08
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                                                                                                                  02-JAN-2003.
(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
(NASC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
22.6%; Score 204.8; DB 10;
ery Match 22.6%; Pred. No. 1.5e-47;
                                                                                                                                                                                                                                                                                                                    02-AUG-2001.
02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
22-6%;
ery Match 22-6%;
917 64milarity 79.6%;
                                                                                                                                                                                ADC87336 standard; DNA; 108316 BP. Human GPCR gene SEQ ID NO:1789. EP1270724-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADQ18538 standard;
Human soft tissue
WO2004048938-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABK83497 standard; cDNA; ;
Human cDNA differentially
WO200228999-A2.
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                                                                                                                                                                                                                                                                          ADJ10262 standard; DNA; 51001 BP. Human geranylgeranyl diphosphate US2004005570-A1.
                                                                                                                                                                                                                                                                                                                                                                                                           29-JUN-1995.
(IMMU-) IMMUNOBIOLOGY RES INST INC.
ry Match
22.6%; Score
76.5%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human thymopoietin WO9517205-Al.
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                                                                                                                                                                                                                                                                                                                                                                               AAS41738 standard; DNA; 32217 BP.
Genomic sequence #54 encoding novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INCY-) INCYTE GENOMICS INC.
ry Match 22.6%;
t Local Similarity 84.7%;
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                                                      AAK86146 standard; DNA; 16997 BP.
Human immune/haematopoietic antigen genomic sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ92781 standard;
                      HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                   ISIS-) ISIS PHARM INC
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gene fragment.
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83.3%;
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84.1%;
SCI INC.
22.6%;
81.8%;
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77.1%;
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73.1%;
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y expressed
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No. 1.
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No. 4e-
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No. 1.
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No. 1.1e-47;
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No.
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No.
 204.6; DB 4;
No. 8.7e-48;
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No.
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No. 1.2e-47;
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.8e-47;
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.8e-47;
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-48;
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               16997;
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RESULT 301
ID AAK800
DE Human
PN WO200:
PD 09-AU
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                                                                         RESULT 309
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 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                     Mammary gland bioreactor related CN1324952-A.
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                                 Human interleukin-11 DNA fragment WO200285309-A2.
                                                                                                                                                                                                                                AAF20955 standard; DNA; 6870 l
Interleukin-11 polynucleotide
WO200062736-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immune/haematopoietic WO200157182-A2.
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(VITI-) VITIVITY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SAGR-) SAGRES DISCOVERY.
(SAGR-) SAGRES DISCOVERY.
22.6%;
ry Match 22.6%;
t Local Similarity 83.2%;
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WO2003073826-A2.
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ry Match 22.6%;
t Local Similarity 81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-SEP-2003
                                                                                                                                           ABZ96649 standard; DNA; 6870
Human interleukin-11 nucleic
                                                                                                                                                                                                                                                                                                                                   AAA34833 standard; DNA; 6870 BP.
Human adenosine receptor related polynucleotide
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                                                                                                                                 WO200285308-A2.
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                                                                                                                                                                                                                                                                                                                        WO200009525-A2.
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                                                                                                         (EPIG-) EPIGENESIS
                     (EPIG-)
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h 22.5%;
Similarity 81.4%;
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                     EPIGENESIS
22.5%;
81.4%;
                                                                                                             PHARM INC.
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82.7%;
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81.8%;
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81.4%;
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81.4%;
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No. 7e-
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No. 7e-
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No.
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No. 1.9e-47;
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No. 7e
  204.4; DB
No. 7e-48;
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2.4e-47;
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3.7e-48;
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-48;
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DE Secreted PD WO20
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RESULT 314
ID AA"
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RESULT 311
ID AAF20956 standard; I
DE Interleukin-11 polyr
PN W0200062736-A2.
PD 26-0CT-2000.
PA (UYEC-) UNIV EAST CA
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RESULT 312
ID ARTOCT
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Query Match
Best Local Similarity
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Human immune/haematopoietic ant:
W0200157182-A2.
O9-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI St;
Duery Match

10cal Similarity 82.7%; Pro-
                                                                           MCZUVIJIII
02-AUG-2001.
02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
22.5%;
ery Match 22.5%;
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09-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
22.5%;
ery Match 22.7%;
                                         Secreted protein gene WO200277013-A2.
                                                                                                                         Human genomic DNA
WO200155449-A1
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Human immune/haematopoietic ar
WO200157182-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABZ96650 standard;
Human nucleic acid
WO200285308-A2.
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                                                                                                                                               AAI62923 standard;
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Human interleukin-11 DNA fragmen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA34834 standard;
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ry Match 22.5%;
t Local Similarity 81.4%;
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TY Match 22.5%;
Local Similarity 81.4%;
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polymucleotide
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22.5%;
y 81.4%;
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   SCI INC.
22.5%;
82.7%;
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22.5%;
82.7%;
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81.4%;
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191 genomic
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No. 9.3
   204.4; DB 8
No. 9.3e-48;
                                                                                   204.4; DB 4;
No. 9.3e-48;
                                                                                                                                                                  No.
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No. 9.3e-48;
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No. 7.4e-48;
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No. 7.4e-48;
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No.
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.3e-48;
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.4e-48;
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                                                    HE8FC45
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Query Match
Best Local Similarity
RESULT 320
ID AAK73099 standard; D
DE Human immune/haemato
PN WO200157182-A2.
PD 09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 322
ID AAK85290 standard; D
DE Human immune/haemato
PN W0200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME
                                                                                                                                       Query Match
Best Local Similarity
RESULT 326

ID ABZ68195 standard; D
DE Human secreted prote
PN W0200277186-A2.
PD 03-OCT-2002.
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
RESULT 324

ID AAI62921 standard, D
DB Human genomic DNA SE
PN W0200155449A1.
PD 02-AUG-2001.
Query Match
Best Local S
RESULT 328
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ID ABZ681
DE Human
PN WO2002
PD 03-OCT
PA (HUMA-
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Best Local Similarity
RESULT 325
                                                                                           Best Local Similarity RESULT 327
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                                                                                                                 Query Match
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                                                       Human cancer-associated WO2004074320-A2.
                                                                                                                                                                                                                                   Secreted protein WO200277013-A2. 03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune/haematopoietic antigen WO200157182-A2.
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ry Match 22.5%;
st Local Similarity 82.7%;
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Human immune/haematopoletic antigen
WOZ00157182-A2.
09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME
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Human immune/haematopoietic antigen
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ry Match 22.5%;
t Local Similarity 82.7%;
                                                                                ABD32665 standard;
                                                                                                                              (HUMA-) HUMAN GENOME
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(HUMA-) HUMAN GENOME SCI INC.
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ry Match 22.5%;
t Local Similarity 82.7%;
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                                  SAGR-) SAGRES DISCOVERY INC.
                                                                                                                                                              ard; DNA; 14426 BP.
protein encoding g
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SEQ ID NO 249.
                                                                  DNA; 112453 E
iated genomic
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82.7%;
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No. 9.3
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             204.4; DB
No. 2e-47;
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No. 9.3e-48;
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9.3e-48;
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9.3e-48;
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9.3e-48;
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9.3e-48;
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9.3e-48;
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Query Match
Best Local S
RESULT 331
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RESULT 330
ID AAF21
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MSI-H carcinoma ger
ABL58149 standard; DNA; 11754 Human ABCA1 transporter gene f WO200236770-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                     ABD17970 standard; DNA; 209284 BP.
Human factor-related antisense polynucleotide.
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(SAGRE) SAGRES DISCOVERY.
(SAGRE) 22.5%;
Local Similarity 81.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EPIG-) EPIGENESIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYEC-) UNIV EAST CAROLINA.
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                                                                                               Human ABC1 gene,
WO200130848-A2.
                                                                                                           AAS04033 standard; DNA; 11754 BP.
Human ABC1 gene, partial genomic
                                                                                                                                                                      (UYBR-) UNIV BRITISH COLUMBIA.
(XENO-) XENON BIORESEARCH INC.
                                                                                                                                                                                                                     AAC69133 standard; DNA; 4736 BP.
Human ABC1 gene exon 2.
                                                                                                                                                                                                                                                                                                                                   BA96807 standard;
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                                               (AVET) AVENTIS PHARMA SA.

CY Match 22.5%;
Local Similarity 80.7%;
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LEE J S.
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DNA sequence.
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9-encoding cDNA
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ed antisense
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80.7%;
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Pred. No. 2.
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Pred. No. 2.6e-47;
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polynucleotide
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                                                                                                              clone
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No. 2.4e-47;
                                                 204
No.
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No. 2.6e-47;
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No. 2.1e-47;
                                                                                                                                                204.2; DB 3;
No. 6.9e-48;
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                                                 9.8e-48;
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2.6e-47;
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4.7e-48;
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Best Local Similarity RESULT 339
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Best Local Similarity
RESULT 337
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RESULT 341
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(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
22.5%; Score 204; DB 10;
ery Match 22.5%; Score 204; DB 10;
et Local Similarity 84.1%; Pred. No. 1.7e-47;
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Human reproductive
WO200155320-A2.
                                                                                                                                                                                                                   ABK48904 standard; DNA; 3635 BP.
Novel human kallikrein KLK15, intron
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADC86460 standard; DNA; 33137
Human GPCR gene SEQ ID NO:913
EP1270724-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human testicular antigen encoding WO200155317-A2.
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ry Match 22.5%;
t Local Similarity 81.6%;
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Human ABC1 genomic
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ry Match 22.5%; Score 204.2;
t Local Similarity 80.7%; Pred. No. 2.6
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                                                                                                      ABK48346 standard; DNA; 8735 BP. Genomic DNA encoding novel human
                                                                                                                                                                                                     Novel human kal
WO200214485-A2.
                                                                                                                                                                                                                                                                                                              Genomic DNA encoding US2003054347-A1.
                                                                                                                                                                                                                                                                                                                                           ACH03435 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
ADN10936 standard; DNA; 8735
Human kallikrein 15 gene, man
                                      (MOUN ) MOUNT SINAI HOSPITAL.
ry Match 22.5%;
t Local Similarity 86.2%;
                                                                                            WO200214485-A2.
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                                                                                                                                                                                                                                                                                                                             DNA; 48840
ng human lat
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DNA.
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) gene, complete cds DNA.
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system related
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22.5%; Score 204.2; DB 6
80.7%; Pred. No. 9.8e-48;
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86.2%;
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84.1%;
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No.
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No. 2.8e-47;
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No. 8.1e-48;
endocrine cancer.
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1.1e-47;
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.9e-47;
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Best Loca
RESULT 350
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RESULT 346
ID ADS36456 standard; I
DE Human autoimmune dis
DN W02004083403-A2.
PD 30-SEP-2004
PA (APPL-) APPLERA CORI
                                                                          Query Match
Best Local Si
RESULT 353
ID AAK87082 E
DB Human immu
PN WO20015718
PD 09-AUG-200
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RESULT 348
ID ADA027
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RESULT
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RESULT 354
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RESULT 351
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30-JAN-2003.

30-JAN-2003.

(SAGR-) SAGRES DISCOVERY.

22.5%;

22.5%;

27.5%;

27.5%;
                                                                                                                                                                       Osteoarthritis-associated polym WO2003054166-A2.
ABZ73865 standard;
Secreted protein ge
WO200277013-A2.
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(SAGR-) 22.5%;
SIXY Match 22.5%;
SIX Local Similarity 79.5%;
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Human VDAC1 carcinoma
WO2003057146-A2.
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Human autoimmune disease-related genomic DNA sequence
WO2004083403-A2.
                                                                                                AAK87082 standard; DNA; 4658 BP.
Human immune/haematopoietic antigen
                                                                                                                                                                     03-JUL-2003
                                                                                                                                                                                                                                                                                     AAD41740 standard; I
Human RECQL2 DNA #1.
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Human VDAC1 gene genomic DNA;
WO2003039484-A2.
                                                                   (HUMA-) HUMAN GENOME
                                                                                         WO200157182-A2.
                                                                                                                                    (INCY-) INCYTE GENOMICS INC.
ry Match 22.5%;
t Local Similarity 78.9%;
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WO2004083403-A2.
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ry Match 22.5%;
t Local Similarity 79.5%;
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          gene
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disease-related
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22.5%;
83.6%;
                      DNA; 18902
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                                          3 SCI INC.
22.4%;
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          71 genomic
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          fragment HCRBF72,
                                          203.6; DB
No. 1e-47;
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No. 1.1e-47;
                                                                                                  genomic
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2.9e-47;
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Θ.
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           NO:1012
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RESULT 356
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Best Local Similarity
RESULT 355
ID ABZ67444 star*
DB Human sec-
PN WO20"
Quer,
Best Lo.
RESULT 363
ID AALOA'
DE Hum
PN W'
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RESULT 357

ID AAK77913 standard; DN
DE Human immune/haematog
PN W0200157182-A2.
PD 09-AUG-2001.
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RESULT 361
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07-SEP-2001.
(HYSE-) HYSEQ INC.
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03-0CT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADD71350 standard; DNA; 93390 BP. Glutamine:fructose-6-phosphate am WC2003023063-A1.
    Human reproductive WO200155320-A2. 02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                               AAK77915 standard; DNA; 646 Human immune/haematopoietic WO200157182-A2.
                                                                                                                                                                        AAK77914 standard; DNA; 2558 Human immune/haematopoietic a
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Human immune/haematopoietic
WO200157182-A2.
09-AUG-2001.
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(SANY ) SANKYO CO LTD.
                                AAL04537 standard;
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ry Match 22.4%;
t Local Similarity 81.6%;
                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
ry Match 22.4%;
t Local Similarity 83.7%;
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ry Match 22.4%;
t Local Similarity 83.7%;
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22.4%;
ty 81.3%;
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                       system related antigen DNA SEQ
                                  DNA; 4067 BP
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system related
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22.4%;
83.7%;
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22.4%;
81.6%;
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79.7%;
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No. 5.4e-48;
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No. 1.7e-47;
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1.1e-47;
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8.5e-48;
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1.7e-
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3.2e-47;
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e-47;
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Best Local Similarity
RESULT 366
ID AAK77916 standard;
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RESULT 365
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02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
(ELMA-) HUMAN GENOME SCI INC.
22.4%;
ery Match 22.4%;
                                                                                                                                                                                                                                                                                                                                                                         AAK89112 standard; DNA; 32190 BP.
Human digestive system antigen ge
WO200155314-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immune/haematopoietic WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immune/haematopoietic WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL97460 standard; DNA; 4067 BP. Human testicular antigen encoding WO200155317-A2.
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                                                                                                                                                                                                                                                                                                AAS31862 standard; DNA; 32190 BP.
Human liver associated genomic DN
                                                                                                                                                                                                                                                                                                                                                    02-AUG-2001.
(HUMA-) HUMAN GENOME
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(HUMA-) HUMAN GENOME
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(HUMA-) HUMAN GENOME
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 ABS69895 standard; DNA; 56: Human hypoxanthine-guanine US2002102731-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001.
(HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK73223 standard;
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                                                                                                                                                                                                          Human liver antigen
                                                                                                                                                                                                                                                                                      WO200155355-A1.
                                                                                      US2003077602-A1.
                                                                                                Human liver-related
                                                                                                          ADJ15130 standard; DNA; 32190
                                                                                                                                                  (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                     ABN90217 standard; DNA;
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(HUMA-) HUMAN GENOME
                                                                 HUMA-) HUMAN GENOME
                                 Local Similarity
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83.7%;
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22.4%; 9
77.9%; 1
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79.1%; 1
                                          3 SCI INC.
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79.1%;
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83.7%;
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           phosphoribosyltransferase
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DNA -
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No. 1.1e-47;
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No. 2.4e-47;
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No.
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No. 2.4e-47;
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1.1e-47;
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2.4e-47;
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ID AAK78°
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RESULT 373
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RESULT 380
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(UYNY) UNIV NEW YORK STATE RES FOUND.
22.4%; Score 203.4;
ery Match 22.4%; Pred. No. 3e-
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                                                                                                                                                                       ABD33276 standard; DNA; 256190 BP.
Human cancer-associated (CA) gene HD07-048
                                                                                                                                                                                                                                                                                                                           WO2003073826-A2.
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09-AUG-2001.
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Human immune/haematopoietic ar
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ry Match 22.4%;
t Local Similarity 83.3%;
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Human neuroblastoma cell line
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ry Match 22.4%;
t Local Similarity 83.8%;
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Human immune/haematopoietic
                      AAK80969 standard;
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                                                                                                                                                     #O2004058146-A2.
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22.4%;
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h 22.4%;
Similarity 75.1%;
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sequence h
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ed with low HDL-C
                          DNA; 6187 BP
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83.0%; Pred.
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No. 6.2e-47;
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No. 4.9e-47;
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2.9e-47;
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3e-47;
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5.6e-47;
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.6e-48;
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-47;
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RESULT 385
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Best Local Similarity
RESULT 390
ID AAK71815 standard; I
DE Human immune/haematc
PN W0200157182-A2.
PD 09-AUG-2001.
                                                                                                                                                                                                                                                 Best Local Similarity
RESULT 387
ID AAL04936 standard; D
DE Human reproductive s
PN W0200155320-A2.
PD 02-AUG-2001.
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Best Local Si
RESULT 386
ID AAD04910 F
DB Human sect
PN W020013479
PD 17-MAY-200
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RESULT 383
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(HUMA-) HUMAN GENOME SCI INC.

22.4%;

27.4%;

27.2%;
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14-JUN-2001.

(MERI ) MERCK & CO INC.

22.4%;

22.4%;

24.1%;
                                                                                                                                                                          ABL97830 standard; DNA; 3753 BP. Human testicular antigen encoding WO200155317-A2.
                                                                                                                                                                                                                                                           AAL04936 standard; DNA; 3753 BP.
Human reproductive system related antigen
WQ200155320-A2.
                                                                                                                                                                                                                                                                                                                                           Human secreted protein-encoding WO200134799-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                   Human cancer associated WO2004060304-A2.
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Human genome from I
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Gene #3429 used to
          Human immune/haematopoietic antigen genomic sequence WO200157182-A2.
                              AAK71815 standard; DNA; 14448 BP
                                                                                                     Human secreted
                                                                                                               AAD04901 standard;
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ry Match 22.4%;
t Local Similarity 74.0%;
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ry Match 22.4%;
t Local Similarity 81.7%;
                                                 (HUMA-) HUMAN GENOME SCI INC.
TY Match 22.4%;
Local Similarity 74.0%;
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protein-encoding g
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diagnose
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22.4%;
79.2%;
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83.7%;
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76.4%;
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gnose liver
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No. 1.3e-47;
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. 1.7e-47;
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.2e-47;
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Query Match
Best Local Similarity
RESULT 399
ID AAS40317 standard; DI
DE DNA encoding human pi
PN WO200155316-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME
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RESULT 395
ID AAK71
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Best Local Similarity
RESULT 392
ID AAK73111 standard; DI
DE Human immune/haematog
PN WO200157182-A2.
PD 09-AUG-2001.
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Best Local Similarity
RESULT 391
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RESULT 394
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RESULT 397
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RESULT 396
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Human immune/haematopoietic antigen
WO200157182-A2.
09-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
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                                                                                                        Human reproductive WO200155320-A2.
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Human genomic DNA SBQ ID
WO200155449-A1.
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Human immune/haematopoietic au
WO200157182-A2.
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Human immune/haematopoietic antigen
WO200157182-A2.
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EXY Match 22.4%;

It Local Similarity 82.4%;
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ry Match 22.4%;
t Local Similarity 82.4%;
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system related
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copoietic antigen
                                 DNA; 22299 BP.
prostate cancer
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Query Match
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RESULT 400
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Human secreted protein encoding gene.
22.4%; Score 202.8; DB 10;
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WO2004028346-A2.
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                                                                                                                                                                                                                                                                                                                     Human nucleic acid WO200285308-A2.
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ry Match 22.4%;
t Local Similarity 83.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA35003 standard; DNA; 56583 BP.
Human adenosine receptor related
                                                                                                                                                                                                                                        ABD20668 standard; DNA; 56583 BP.
Human pulmonary and inflammatory
                                                                                                                                                                                                                                                                                               31-OCT-2002.
(EPIG-) EPIGENESIS PHARM INC.
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Human low adenosine antisense
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WO2003073826-A2.
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ry Match 22.4%; Score 20
t Local Similarity 78.9%; Pred. N
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                                              WO2004048938-A2.
                                                                   ADQ17329 standard;
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  PROTEIN DESIGN LABS

1 22.4%;
Similarity 79.2%;
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22.4%;
83.4%;
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sequence.
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                         INC.
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Pred. No. 3.4e-47;
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oligonucleotide
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No. 3.2
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No. 3.2e-47;
   202
No.
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No. 4.5e-47;
                                                                                         202.8; DB 1
No. 5.6e-47;
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No.
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No. 4.5e-47;
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                                                           DNA
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   .8; DB 12;
5.7e-47;
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4.5e-47;
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.2e-47;
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Best
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02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
22.3%;
27. Match
22.3%;
83.1%;
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DNA (SeqID 4) related to the
                                                                                                                                                                                                                                                                                                                                                                                                               wo200224921-A2.
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WO2003073826-A2.
                                                            ADL30885 standard; cDNA; 3395 Full length human cDNA clone (EP1396543-A2.
                                                                                                                                                            AAK94280 standard;
Human full-length c
                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK14000 standard; cDNA;
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ry Match 22.3%;

t Local Similarity 81.7%;
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Human TGF-beta receptor cDNA clone
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ry Match 22.4%;
t Local Similarity 76.0%;
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                                                                                                                                                   EP1130094-A2.
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                                                                                                                                                                                                                                               Human kinase
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                                         (REAS-) RES ASSOC BIOTECHNOLOGY
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CDNA; 3443
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No. 1.7
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No. 1.
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No. 1.7e-47;
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No. 6.3e-47;
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1.7e-47;
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1.7e-47;
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1.7e-47;
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RESULT 425
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RESULT 420
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PN WO2'
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PD 15
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BESULT 423
ID ABA
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RESULT 422
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Best Local Similarity
RESULT 426
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RESULT 419
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RESULT 421
ID ADO20171 standard;
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W0200157182-A2.
09-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
Match 22.3%; So
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Human cardiovascular system antiger
W0200155321-A2.
02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI SCORE
DUCTY MATCH
22.3%; Score
Lest Local Similarity 85.6%; Pred.
                                                                                                     Human standard; DNA; 20869
Human immune/haematopoietic an
WO200157182-A2.
09-AUG-2000
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                             Human nervous system WO200159063-A2.
                                                 ABA16245 standard;
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                                                                                                                                                                                                                                                                                               ABA20357 standard;
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Human immune/haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADF81952 standard;
Leukaemia-related
WO2003039443-A2.
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                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
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                                                                                         (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
(UYLU-) UNIV LUDWIG MAXIMILIANS.
(HAFE/) HAFERLACH T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH
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No. 1.8e-47;
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3.5e-47;
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1.8e-47;
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Best Local Similarity
RESULT 427
ID ADE47621 standard; D.
DE Human cardiovascular
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME
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RESULT 432
ID AAS36105 standard; D
DB Human cardiovascular
PN W0200155321-A2.
PD 02-AUG-2001.
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RESULT 431
ID AAK66126 standard; D
BE Human immune/haemato
PN W0200157182-A2.
PD 09-AUG-2001
PA (HUMA-) HUMAN GENOME
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RESULT 433
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                                         Genomic DNA encoding WO200155318-A2.
                                                                                                                     Human DNA for a novel extracellular matrix WO200155368-A1. 02-AUG-2001.
                                                                                                                                                                                                                       AAS31538 standard; DNA; 32195 BP.
Human DNA for a novel extracellular
WO200155368-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADE47621 standard; DNA; 20869 BP. Human cardiovascular system related
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                                                                  ABK44045 standard;
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Human cardiovascular system antigen
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(HUMA-) HUMAN GENOME SCI INC.
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09-AUG-2001.
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Human immune/haematopoietic
                      (HUMA-) HUMAN GENOME
                                                                                      (HUMA-) HUMAN GENOME SCI INC.
ry Match 22.3%;
t Local Similarity 79.9%;
                                                                                                                                                        AAS31532 standard; DNA; 32195 BP
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                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
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ry Match 22.3%;
t Local Similarity 82.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immune/haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAK82338 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JAN-2004
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Local Similarity
                                                    ng novel cen
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opoietic antigen
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22.3%;
85.6%;
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22.3%;
85.6%;
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82.6%;
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81.7%;
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79.9%;
22.3%;
79.9%;
                    SCI INC.
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c antigen
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                                                                  BP.
 202.4; DB 4;
No. 4.8e-47;
                                                                                       202.
No.
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No.
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No.
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No. 4.9e-47;
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4.8e-47;
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.8e-47;
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-47;
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-47;
                                                                                       DB 4;
e-47;
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          Length 32195;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO:20937.
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Query Mat
Best Loca
RESULT 439
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RESULT 437
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RESULT 438
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                                                                                                                                       Best Local Similarity
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(HUMA-) HUMAN GENOME SCI INC.
22.3%;
2Y Match 22.3%;
27.7%;
                                                                      Human periodontal disease related gene COL18A1 SEQ ID NO:115.

ary Match 22.3%; Score 202.4; DB 13; Length 34079;
bt Local Similarity 81.2%; Pred. No. 4.9e-47;
                                                                                                                                    Human cardiovascular system associated US2004005575-A1.

08-JAN-2004.

(HUMA-) HUMAN GENOME SCI INC.

12.3%; Score 202.

15 Local Similarity 79.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                             Human cardiovascular US2003059908-A1.
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Human polynucleotide SE
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US2002042386-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ADE46799 standard; DNA; 32195 BP.
Human cardiovascular system related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2003059875-A1.
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Human DNA from extracelluar matrix gene 113 #1.
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                                                                                                             ACN37205 standard; DNA; 34079 BP.
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                   AAK83781 standard; DNA; 37664 BP.
Human immune/haematopoietic antigen
                                                                                                                                                                                                                     ADJ08217 standard; DNA; 32195 BP.
                                                                                                                                                                                                                                                                    (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                          JS2004018969-A1.
                                                                                                                                                                                                                                                                                                                                       Novel human protein
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HUMAN GENOME SCI
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22.3%; 5
79.9%; 1
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79.9%; 1
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79.9%;
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79.9%;
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Q ID NO 617
INC
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Pred.
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Pred. No. 4.8e-47;
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Pred.
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No. 4.8
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No. 4.8
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No.
                                                                                                                                          202.4; DB 13;
No. 4.8e-47;
                                                                                                                                                                                                                                              202.4; DB 12;
No. 4.8e-47;
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                                    genomic sequence SEQ ID NO:38593.
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4.8e-47;
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1.8e-47;
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Query Match
Best Local Similarity
RESULT 445
ID ADD19777
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                                      Best Loca
RESULT 453
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Human cancer-associated genomic DNA HD17-008
Human genomic sequence hCG15773. WO2003073826-A2.
                                                                                                                                                                                                                                                                     AAF63405 standard; DNA;
Human CD39 like protein
                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                           Human CD39-L4 genomic DNA.
WO200004041-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAL57580 standard;
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ry Match 22.3%;
t Local Similarity 81.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immune/haematopoietic antigen WO200157182-A2.
                                                                     WO200110205-A1.
15-FEB-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                         AAF63406 standard; DNA;
Human CD39 like protein
WC200110205-A1.
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15-FEB-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAK83782 standard;
                                                                                                    AAF63407 standard; DNA; 15977 BP.
Human CD39 like protein CD39-L4 genomic
                                                                                                                                                                                                                                                                                                                                   27-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0-JUN-2004
                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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activating protein-like
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78.6%;
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CD39-L4 9
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CD39-L4
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No.
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No. 5e-
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No. 3.
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No.
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No. 6.1e-47;
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No.
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No. 3.4e-47;
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No. 8.1e-47;
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5.3e-47;
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4e
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                                                              Length 15977;
                                                                                                                                             Length 14747;
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                                                                                                                                                                                                                                                                                                                                                                                                  Length 129381;
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                                                                                                       #2
                                                                                                                                                                                                                                9365;
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HESULT 457
ID ADST
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RESULT 455
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Best Local Similarity
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Gene #3429 used to
WO200229103-A2.
                                              (REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                      Human cDNA of EP1347046-A1.
                                                                                ADM02980 standard;
Human cDNA of the
                                                                                                                                                        Human cDNA from WO2003052377-A2.
                                                                                                                                                                                                                    26-JUN-2003.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                          Human cDNA from secreted WO2003052377-A2.
                                                                                                                                                                                                                                                                                                                                                                  ACH25975 standard; cDNA; 502
Human adult ovary cDNA #4355.
US2003073623-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human housekeeping gene cDNA sequence WO2004035785-A1.
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(SAGR-) SAGRES DISCOVERY.

22.3%;

TO Match 22.3%;

83.2%;
         ADD18777 standard;
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                                                                                                                                                                  ADD19217 standard; cDNA;
Human cDNA from secreted
                                                                                                                                                                                                                                                              ADD19251 standard;
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ry Match 22.3%;
t Local Similarity 82.1%;
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                                                                                                                                    (HUMA-) HUMAN GENOME
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ry Match 22.3%;
t Local Similarity 82.1%;
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                                                                                                                                                                                                                                                                                                     (LABA/) LABAT I.
(STAC/) STACHE-CRAIN B.
(DICK/) DICKSON M C.
(JONE/) JONES L W.
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                              Local Similarity
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dard; DNA; 8672 BP.
related protein DNA sequence SeqID208.
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22.3%;
7 79.5%;
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invention SE
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diagnose li
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gene cDNA #96.
                                                                                                                                                                                                                                                              CDNA;
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                                                                                                              3 SCI INC.
22.3%;
81.5%;
                              22.3%;
78.2%;
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81.5%;
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protein
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SEQ ID
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No. 1.5e-
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No. 2.
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No. 1.
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No.
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No.
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No. 1.2e-47;
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No.
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No. 5.3e-47;
                                                                                 NO:1665
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8.7e-47;
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9.1e-47;
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Best Local Similarity RESULT 471
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Best Local Similarity
RESULT 467
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Best Local Similarity
RESULT 465
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RESULT 463
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04-APR-2002.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
22.3%;
pery Match 22.3%;
                                                                                                                                                                                                                                              Secreted protein gene 12 genomic W0200276488-Al. 03-OCT-2002.
Human secreted I
WO2003004622-A2
                                                                                             ADB91835 standard; DNA; 15090 I
Human secreted protein related
                                                                                                                                                                                  Secreted
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                                                                                                                                                                                              ABZ71479 standard; DNA; 15090
                                                                                                                                                                                                                                                                                                                                                                     ACC50858 standard;
         ADB91836 standard; DNA; 15090 |
Human secreted protein related
                                                                         WO2003004622-A2.
16-JAN-2003.
                                                                                                                                                                         WO200276488-A1.
                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
ry Match 22.3%;
t Local Similarity 83.0%;
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ry Match 22.3%;
t Local Similarity 83.0%;
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Human secreted protein gene 22
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ry Match 22.3%;
t Local Similarity 83.0%;
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ry Match 22.3%;
Local Similarity 83.0%;
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                                                              (HUMA-) HUMAN GENOME
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protein gene 12 genomic
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                                       SCI INC.
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74.6%;
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No. 4.6e-47;
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16-JAN-2003

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Best Local Similarity
RESULT 479
ID ADDR2368 standard; Di
DE Human FLT3 gene.
PN W02003008583-A2.
PD 30-JAN-2003
PA (SAGR-) SAGRES DISCOV
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RESULT 472
ID ADC74610 standard; DE Human secreted prote
PN W02003038063-A2.
PD 08-MAY-2003.
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RESULT 473
ID ADC74611
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RESULT 477
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        ADE95878 standard; DNA; 32433 Human FLT3 gene genomic DNA se WO2003039484-A2.
                                                                                                                                                                                       ADA02630 standard; DNA; 32433
Human FLT3 carcinoma associate
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BAC fragment containing human
                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA clone in ATCC
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                                                 (SAGR-) SAGRES DISCOVERY.
ry Match 22.3%;
t Local Similarity 80.3%;
                                                                                                                                                                                                                                                                                                                               HUMA-) HUMAN GENOME SCI INC.
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protein-related
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deposit #24.
                                                                                                               DNA; 32433
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22.3%;
83.0%;
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83.0%; )
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.6e-47;
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.6e-47;
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.6e-47;
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.2e-47;
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Query Match
Best Local Similarity
RESULT 481
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RESULT 485
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Best Local Similarity
RESULT 483
                      Best Local Similarity RESULT 489
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RESULT 487
ID AAL07205 standard;
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WO200155367-A1.
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                                                                                                cDNA encoding novel US2002147140-A1.
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ry Match 22.2%;
t Local Similarity 81.0%;
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Human immune/haematopoietic antigen
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                                                     (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C
                                                                                                                       ABX59565 standard;
                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC ry Match 22.2%; t Local Similarity 76.9%;
                                                                                                                                                                                                                                                                                                                                                                      DNA encoding human WO200155326-A2.
                                                                                                                                                                                                                                                                                                                                                                                           AAS33461 standard;
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Novel human cDNA sequence #1595.
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ry Match 22.2%;
t Local Similarity 78.1%;
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ADJ30315 standard; DNA; 11991
Human musculoskeletal system-a
                                                                                                                                                                             02-AUG-2001
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                                                                                                            cDNA; 11991 BP.
l human musculoskeletal
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No. 1.3e-46;
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No. 8.3e-47;
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No. 6.2e-47;
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No. 4.8e-47;
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3.4e-47;
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4.8e-47;
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4.4e-47;
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15-JAN-2004

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W0200155326-A2.
02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
22.2%; S'
22.2%; S'
31.0%; P
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15-JUL-2004.
(SAGR-) SAGRES DISCOVERY INC.
22.2%;
27 Match
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29 Match
29 Match
20 Ma
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Prostate and breast cancer as
WO2004028346-A2.
08-APR-2004.
(AMSH ) AMERSHAM BIOSCIENCES
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                                 (SAGR-) SAGRES DISCOVERY.

"Y Match 22.2%;

It Local Similarity 79.9%;
                                                                                                                                                                                                                                                                                 ADL13775 standard; DNA; 173805 BP. Osteoarthritis-associated polymorphic WO2003054166-A2.
ADE43315
                                                                                                                                        ACN44626 standard; DNA; 175077 B
Human genomic sequence hCG19724.
                                                                                                                                                                                                 (INCY-) INCYTE GENOMICS INC.
ry Match 22.2%;
t Local Similarity 83.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cancer-associated WO2004058146-A2.
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Human cancer-associated (CA) gene
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standard; DNA; 202100
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cancer ası
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secreted protein,
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81.0%;
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No. 1.3
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No. 1.3e-46;
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No. 1.1e-46;
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No. 4.8e-47;
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                                       1.4e-46;
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3.2e-47;
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.9e-47;
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RESULT 503
ID ADROF
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RESULT 505
ID AAI57794 standard; D:
DE Human colorectal can-
PN W0200155350-A1.
PD 02-AUG-2001.
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RESULT 500
ID ADH54357 standard; DN
DE Human IDE/KNSL1 gene
PN US2003224380-A1.
PD 04-DEC-2003.
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US2003224380-A1.
04-DEC-2003.
(GEHO ) GEN HOSPITAL C
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17-APR-2003.
(GENO-) GENOME THERAPEUTICS (GENO-)
ery Match 22.2%;
ery Match 83.7%;
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Human genomic DNA
WO200155319-A2.
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                                                                           ABS99971 standard; DNA; 8896 BP. Genomic DNA #175 encoding human
                                                                                                                                                        Human genomic DNA WO200155319-A2.
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Human colorectal cancer antig
WO200155350-A1.
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WO2003031594-A2.
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Human IDE/KNSL1 gene DNA sequence SeqID484
                                                                 US2002119919-A1.
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ry Match 22.2%;
t Local Similarity 77.7%;
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ry Match 22.2%;
t Local Similarity 77.7%;
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                       (BARA/)
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CY Match 22.2%; Score
Local Similarity 83.0%; Pred.
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No. 1.6e-46;
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201.6; DB 6;
No. 4.9e-47;
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No. 4.9e-47;
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3.5e-47;
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Best Local Similarity
RESULT 510
ID AAL60676 standard; D
DE DDC353 knockout cons
PN W02003044214-A2.
PD 30-MAY-2003.
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RESULT 514
ID AAI99173
DE Human exc
PN WO2001553
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30-MAY-2003.
(BAYU ) BAYLOR COLLEGE MEDICINE.
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(HUMA-) HUMAN GENOME
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AAK84138 standard; DNA; 17758 BP.
היישים immune/haematopoietic antigen
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Human kidney related polynucleotide
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Human immune/haematopoietic an
                                                                                                        02-AUG-2001.
(HUMA-) HUMAN GENOME
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(HUMA-) HUMAN GENOME
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ry Match 22.2%;
t Local Similarity 77.7%;
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cancer related
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07-FEB-2001.
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Human cDNA sequence SEQ ID
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Human sequence from
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ry Match 22.2%;
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Human immune/haematopoietic antigen
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                 Human MHC class
WO9819167-A2.
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WO2003072827-A1.
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(STAC/) STACHE-CRAIN
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8.3e-47;
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1.3e-47;
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.6e-47;
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.5e-46;
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RESULT 526
ID ADE06443 :
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RESULT 532
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Human nervous system related polynu
W0200159063-A2.
16-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI SCORE
DIETY MATCH
22.2%; Score
EBE Local Similarity 85.0%; Pred.
                                                                                                                                                             Human genomic sequence hCG24994. WO2003073826-A2.
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02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
22.2%;
ery Match 22.2%;
ery Match 81.2%;
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(HUMA-) HUMAN GENOME SCI INC.
(EXPRESS OF THE SCI INC.
22.2%;
ery Match 22.2%;
ery Match 81.2%;
                                   Human kinase
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                                                                                                                                                                                                                                                                                                                          08-APR-2003
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ry Match
Local Similarity 81.2%;
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CY Match 22.2%;

Local Similarity 81.2%;
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C
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83.6%; Pred.
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Best Local Similarity
RESULT 543
ID AARTIC
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RESULT 538
ID ABL67239 standard; D
DE .Thyroid cancer relat
PN W0200194629-A2.
PD 13-DEC-2001.
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Human immune/haematopoietic WO200157182-A2.
                                                                                AAK71817 standard; DNA; 14426 Human immune/haematopoietic au WO200157182-A2.
                                                                                                                                                                     AAK87586 standard; DNA; 14426 BP. Human immune/haematopoietic antigen WO200157182-A2.
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07-FEB-2001.
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                 AAK73115 standard;
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                                                             (HUMA-) HUMAN
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No. 1.7e-46;
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03-OCT-2002.
(HUMA-) HUMAN GENOME SCI INC.
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(HUMA-) HUMAN
        AAK65169 standard; DNA; 370 BP. Human immune/haematopoietic antigen W0200157182-A2.
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Human immune/haematopoietic antigen
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ry Match 22.2%;
t Local Similarity 82.1%;
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(SAGR-) SAGRES DISCOVERY INC.
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09-AUG-2001.
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ry Match 22.2%;
t Local Similarity 82.1%;
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ry Match 22.2%;
t Local Similarity 76.6%;
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ry Match 22.2%;
t Local Similarity 81.4%;
                                         ABD33084 standard; DNA; Human cancer-associated
                                                                                                     Human transporter WO200248367-A2.
                                                                                                                          AAD44328 standard; DNA; 34667
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Human immune/haematopoietic antigen genomic
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ry Match 22.2%;
t Local Similarity 78.7%;
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Human immune/haematopoietic antigen
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Human calcium/calmodulin-dependent
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ry Match 22.2%;
t Local Similarity 81.4%;
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1 (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

1 (AAD-) NAT ADVANCED SCI & TECHNOLOGY INCUBATIO.

1 (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

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(SAGR-) SAGRES DISCOVERY.
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(INCY-) INCYTE GENOMICS INC.

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Human GPCR related
EP1270724-A2.
                  ACH29888 standard; cDNA;
Human testis cDNA #274.
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(MCLA-) MCLAUGHLIN
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Osteoarthritis-associated polymorphic nucleotide
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t Local Similarity 77.2%;
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                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA; 144792 BP. polynucleotide
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                                                                                                                                                                                                                                                                                                                                  RES INST.
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81.4%;
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78.7%;
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78.
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k; Score 201; DB 10;
k; Pred. No. 2.1e-46;
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Pred.
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No. 2
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No. 2.
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No. 1.
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No. 1.
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No. 2e-46;
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No. 1.6e-46;
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..3e-46;
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.3e-46;
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                                                                                                                                                                                                                                                                                          6e
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AUG-2001.

(HUMA-) HUMAN GENON
QUETY MATCH
Best Local Similarity
RESULT 579
ID AAK66931 stand*
DB Human immur
PN W020015*
PD 09-
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RESULT 575
ID AAL05495 standard; DN
DE Human reproductive sy
PN W0200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME
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RESULT 573
ID ABS57269 standard; DN
DE Partial sequence #3 c
PN US6451763-B1.
PD 17-SEP-2002.
PA (USSH ) US DEPT HEALT
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ID ADB990
DB Human
PN US2003
PD 22-WAY
PA (TOMB/
PA (STEE)
PA (CHAD)
PA (BECE)
PA (RODR/
PA (RODR/
                                                                                                                                                      Best Local Similarity RESULT 578
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(STAC/) STACHE-CRAIN E
(DICK/) DICKSON M C.
(JONE/) JONES L W.
                                                                                                                     Human testicular antigen WO200155317-A2.
                                                                                                                                                                                                                                                                                  Human reproductive system rel
WO200155320-A2.
02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human digestive WO200155314-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USSH) US DEPT HEALTH & HUMAN SERVICES.

22.1%; Score 200.8; DB 10;

t Local Similarity 80.7%; Pred. No. 6.4e-47;
                                                                                                                                             ABL98348 standard;
                                                                                                                                                                                                              Human testicular antigen WO200155317-A2.
                                                                                                                                                                                                                                       ABL97878 standard;
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Human digestive system antigen ge
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Partial sequence #3 of genom:
                                        Human immune/haematopoietic
                                                                                                                                                                                                                                                                                                                                AAL04985 standard;
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Human retinal pigment epithelial-derived
                                                  AAK66931 standard; DNA; 30620
                                                                         (HUMA-) HUMAN GENOME SCI INC.
ry Match 22.1%;
t Local Similarity 79.9%;
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ry Match 22.1%;
t Local Similarity 79.9%;
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CHADER G J.
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                                                                                                                                DNA; 22645 BP.
ntigen encoding
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system related
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22.1%;
79.9%;
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22.1%;
79.9%;
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79.9%;
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80.7%;
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84.6%;
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n encoding
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                                                                         200.8; DB 4;
No. 1.2e-46;
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No.
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No. 1.2e-46;
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No.
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No. 1.2e-46;
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No. 6.4e-47;
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1.2e-46;
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2.5e-47;
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                                          NO:21743
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HUMAN GENOME SCI

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Query Match
Best Local Similarity
RESULT 580
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                                                                                                                                                                                                                                                                                                                                                         MRP1 based cancer related nucleic WO2003013533-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACF62733 standard; DNA; 172984 Cancer based on CYP3A5 related WO2003013534-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADE95848 standard; DNA; 96593 Human RUNX1 gene genomic DNA; WO2003039484-A2.
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                                                                                                                                                                   ADB96920 standard;
Human MDR1 related
WO2003013537-A2.
                                                                                                                                                                                                                                                      Human UGT1A1 gene
WO2003013536-A2.
20-FEB-2003.
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ry Match 22.1%;
t Local Similarity 85.8%;
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(EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
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                                                                                                                                                                                                                                                                                                                   (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
ry Match 22.1%; Score 200.8; DB 8
t Local Similarity 84.9%; Pred. No. 2.6e-46;
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(SAGR-) SAGRES DISCOVERY.
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                                                                       WO2003013535-A2.
                                                                                              ADB92111 standard;
                                                                                                                  (EPID-) EPIDAUROS BIOTECHNOLOGIE
CY Match 22.1%; Scor
Local Similarity 84.9%; Pred
                                                                                                                                                                                                                   (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
ry Match 22.1%; Score 2
Local Similarity 84.9%; Pred. N
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                      ocal Similarity
                                             EPIDAUROS
standard;
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                     BIOTECHNOLOGIE AG.
22.1%; Score 200.8; DB 1
9 84.9%; Pred. No. 2.6e-46;
                                                                                                                                                                                                                                                                               DNA; 172984 BP.
sequence SEQ ID NO:661.
                                                                                                                                                                                DNA;
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DNA;
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85.8%;
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sequence SEQ
                                                                             172984 BP.
  176771 BP
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Pred.
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Pred.
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Pred.
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Pred.
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Pred. No. 2.6e-46;
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Pred. No. 2.1e-46;
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polynucleotide
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No.
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No. 1.3e-46;
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No.
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).8; DB 4; Le
2.2e-46;
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2.1e-46;
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2.1e-46;
                                                                                                                      .8; DB 1
2.6e-46;
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                                                                                    NO:661.
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                                    DB 10;
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    complementary
Length 107820;

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Best Loca
RESULT 596
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                         Best Local Similarity
RESULT 598
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RESULT 592
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RESULT 595
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                                             Query Match
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                                                                                                                                         Connective tissue related genomic US2003054375-A1.
                                                                                                                                                                                                                                                                                                                                                                               Human immune/haematopoietic WO200157182-A2.
Human genomic se
WO2003073826-A2
                                                                       Human autoimmune disease-related WO2004083403-A2.
                                                                                                                                                                                                         (HUMA-) HUMAN
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                                                                                                                                                                                                                                                                                                     AAS32797 standard;
Human genomic DNA
WO200155319-A2.
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                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                              02-AUG-2001
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ry Match 22.1%;
t Local Similarity 84.2%;
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ry Match 22.1%;
t Local Similarity 83.3%;
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                  ACN45210 standard;
                                                                                           ADS36489 standard; DNA; 14902
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                                                                                                                                (HUMA-) HUMAN
                                                       (APPL-) APPLERA CORP.
                                                                                                             ocal Similarity
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      ndard; DNA;
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13q31-q33 genc
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a associated
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22.1%;
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83.0%;
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No. 9.5
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.47;
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Best Loca
RESULT 606
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RESULT 605
ID ADJ79961 standard; Di
DE Full length human gl:
PN WC2003008549-A2.
PD 30-JAN-2003.
          Query Match
Best Local S
RESULT 608
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RESULT 604
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RESULT
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RESULT
ID AL
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Best Local Similarity
RESULT 599
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RESULT 602
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17-JUL-2003.
(SAGR-) SAGRES DISCOVERY.
22.1%;
PATY Match 22.1%;
                                                                                                                                                                         ACN44758 standard; DNA; 172569 BP. Human genomic sequence hCG20145. WO2003073826-A2.
                                                                               ABQ88207 standard; cDNA; 172570 BP. Human osteoblast differentiation re WO200250301-A2.
                                                                                                                                                                                                                                                                                                                                                               ADA66352 standard; DNA; 96596 Human PPP3CC gene genomic DNA WO2003053224-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADB72806 standard;
Human PPP3CC gene.
WO2003008583-A2.
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Human genomic sequence f
US2003216558-A1.
20-NOV-2003.
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 ADL13512 standard;
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ry Match 22.1%;
t Local Similarity 79.4%;
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ry Match 22.1%;
t Local Similarity 81.6%;
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(SAGR-) SAGRES DISCOVERY.
CY Match 22.1%;
Local Similarity 81.6%;
                                            (GENE-) GENE LOGIC INC.
(PROC ) PROCTER & GAMBLE CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MORR/) MORRIS D W.
(ENGE/) ENGELHARD E
                                                                                                                                                                                                                                               ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                               0-JAN-2003
                                                                                                                  Local Similarity 607
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                       Local Similarity
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glioma-associated oncogene-3
DNA; 178870
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                       22.1%;
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85.5%;
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81.4%;
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84.2%;
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for PPP3CC
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No. 3e-46;
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No.
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No. 2.4e-46;
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No. 1.9e-46;
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No. 1.9e-46;
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No. 2.4e-46;
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2.4e-46;
                       3e-46;
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2.4e-46;
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.5e-46;
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Query Match
Best Local Similarity
RESULT 611
                        RESULT 617
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RESULT 616
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RESULT 614
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Best Local Similarity
RESULT 612
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RESULT 610
ID ABL41258 standard;
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Best Local Similarity
RESULT 609
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ADM28896 standard; DNA; 13677 BP.
Human pseudogene #3 located near CYP2D6 gene
                                                                                                 ADJ78568 standard; DNA; 13677
Human cytochrome P450 isoenzym
                                                                                                                                                                                     Human pseudogene US2004072235-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding human WO200224721-A1.
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07-FEB-2001.
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                                                                                                                                                                                                                                                                                                 ADJ78567 standard; DNA; 13278 BP.
Human cytochrome P450 isoenzyme 2
                                                                                                                                                                                                                                                                                                                                                                                                ADQ64569 standard;
Novel human cDNA se
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:ry Match 22.1%;
t Local Similarity 83.7%;
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Human cDNA sequence SEQ ID NO:13234.
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Y Match 22.1%;

t Local Similarity 83.0%;
                                                                                                                                                          (DAWS/) DAWSON E P.
                                                                                                                                                                           15-APR-2004
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Human cytochrome bcl compound
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ry Match 22.1%;
t Local Similarity 83.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABK69090 standard;
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                                                                                                                                                                                                                                      (BIOV-) BIOVENTURES INC.
ry Match 22.1%;
Local Similarity 80.2%;
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                                                             BIOV-) BIOVENTURES
                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  cDNA sequence
                                                                                                                                                                                                  #2 located near CYP2D6
                                                                                                                                                                                                                                                                                                                                                                                                  cDNA; 3341 BP.
equence #1730.
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                                     INC.
22.1%;
80.2%;
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78.2%;
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85.2%;
                                                                                                                                    22.1%;
                                                                                                isoenzyme 2D6
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Pred. No.
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Pred.
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No. 3.5
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No.
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No. 1.3
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No.
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No. 1.3e-46;
                                                                                                 pseudogene
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                                      1.3e-46;
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                                                                                                                                     .4; DB 12;
1.3e-46;
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                                                                                                                                                                                                  gene
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.7e-47;
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                                                DB 12;
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Juery Loc.
Best Loc.
RESULT 626
ID ACN4'
DE HOPE
PN
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RESULT 623
ID AAI72317 standard; cl
DE Human transporter pri
PN W0200202635-A2.
PD 10-JAN-2002.
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RESULT
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O2-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
22.1%;
ery Match 22.1%;
ery Match 22.5%;
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Human reproductive
WO200155320-A2.
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(HUMA-) HUMAN GENOME SCI INC.
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22.1%;
22.5%;
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(DAWS/) DAWSON E P.
Human genomic sequence hCG19724.
WO2003073826-A2.
                                                                                                                                                                                            ABD32649 standard; DNA; 102790 E Human cancer-associated genomic WO2004074320-A2.
                                                                                                                                               (SAGR-) SAGRES DISCOVERY INC.
ry Match 22.1%;
t Local Similarity 82.3%;
                                                                                                                                                                                                                                                                                                                AAI72317 standard; cDNA; 26657
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TY Match 22.1%;
Local Similarity 82.5%;
                                                     (SAGR-) SAGRES DISCOVERY INC.
ry Match 22.1%;
t Local Similarity 85.2%;
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system related
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80.9%;
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No. 1.5
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No. 1.5e-46;
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No. 1.5e-46;
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No. 1.5e-46;
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No. 1.3e-46;
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No. 1.7e-46;
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No. 1.5e-46;
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No. 2.8e-46;
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3.3e-46;
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Query Match
Best Local Similarity
RESULT 627
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Best Local Similarity
RESULT 628
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                                                                                                                   Best Local Similarity RESULT 634
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22.1%;
st Local Similarity 82.3%;
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                                                                          Human immune/haematopoietic a w0200157182-A2.
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                                                                                                                                                                                                                                                                                                                                                 AAK71508 standard; DNA; 781 Human immune/haematopoietic WO200157182-A2.
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22.1%;
ry Match 22.1%;
t Local Similarity 82.5%;
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                                                                                                                                                                       Human immune/haematopoietic WO200157182-A2.
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                      AAK85916 standard;
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ry Match 22.1%; 
t Local Similarity 80.7%;
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ry Match 22.1%;
t Local Similarity 82.5%;
Human immune/haematopoietic antigen
WQ200157182-A2.
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                      DNA; 4553 BP
                                          3 SCI INC.
22.1%;
78.5%;
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80.7%;
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78.5%;
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antigen
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antigen genomic
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No. 4.9e-47;
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3.8e-46;
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4.4e-47;
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Query
Best Lock
RESULT 637
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DE Hump
PN WO'
PD '
PA '
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RESULT 643
ID ADDITIONAL TO THE PROPERTY OF THE PROPERTY
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ID AD
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RESULT 644
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Best Local Similarity
RESULT 641
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RESULT
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(HUMA-) HUMAN GENOME SCI INC.

STY MATCH

12.1%; Scor 22.1%; Pred
ABD33260 standard; DNA; Human cancer-associated WO2004058146-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACN44118 standard; DNA; 31652 BP. Human genomic sequence hCG23908. WO2003073826-A2.
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                                                                                                                                                                                      ADS36454 standard; DNA; 58337 BP.
Human autoimmune disease-related genomic
                                                                                                                                                                                                                                                                                                                                                           ADC87688 standard; DNA; 37138
Human mammalian target of rapa
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WO2003004623-A2.
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                                                                                                                           (APPL-) APPLERA CORP.
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12-JUN-2003.
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ry Match 22.1%;
t Local Similarity 70.8%;
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ry Match 22.1%;
t Local Similarity 81.1%;
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Human neuroblastoma cell line
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No.
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No. 2.2e-46;
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No. 2e-46;
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No. 1.9e-46;
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No. 1.5e-46;
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No. 1.3e-46;
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1.9e-46;
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LUERY MATCH
Best Local Similarity
RESULT 653
ID ACM44966 stand DE Human genomen W02003 no PD 12 PA
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LUGR-) SAGRES DIS.

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RESULT 645

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RESULT 652
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(SAGR-) SAGRES DISCOVERY INC.
                       Human genomic sequence WO2003073826-A2.
                                                                                                              Human kinesin-like
                                                                                                                                                                                             ADS19854 standard; DNA; 113604
Human chromosome 21 nucleotide
WO2004018701-A2.
04-MAR-2004.
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Human LQTS genomic
US2003077633-A1.
                                                                                                                           AAC66548 standard;
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Human chromosome 21 nucleotide
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Human PCTA-1 genomic DNA, SEQ ID N
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ry Match 22.1%;
t Local Similarity 78.8%;
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COXD/) COX D R.
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disease-related
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SAGRES DISCOVERY

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12-SEP-2003.
12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
22.1%;
22.1%;
25.5%;
27.5%;
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Human gene associated with low
US2004043389-A1.
                                                                                                                                                                                                                                                                                                                                                    ADO26258 standard; DNA; 1061 BP.
C35 promoter and polynucleotide targeting method related human DNA
WO2004037993-A2.
                                                                                                                                                                                                                                                                                                                                                                                                  (SAGR-) SAGRES DISCOVERY INC. (SAGR-) SAGRES DISCOVERY INC. 22.1%;
EY Match 22.1%;
83.0%;
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ADO26270 standard; DNA; 7401 BP.
C35 promoter and polynucleotide targeting method related human DNA #12.
                                                                                          Human nucleotide CN1347989-A.
                                                                                                        ABQ83751 standard; cDNA; 1812 BP.
Human nucleotide reductase 16.83
                                                                                                                                                                                                                       ADO26269 standard; DNA; 1107 Human breast cancer associate WO2004037993-A2.
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(SAGR-) SAGRES DISCOVERY.
ry Match 22.1%;
t Local Similarity 83.0%;
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(VITI-) VITIVITY INC.
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                                                                                                                                                                    (UYRP ) UNIV ROCHESTER.
(ZAUD/) ZAUDERER M.
(PARI/) PARIS M.
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(ZAUD/) ZAUDERER M.
(PARI/) PARIS M.
                                          Local Similarity
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                                        DEV CO LTD SHANGHAI.
22.1%; Score 200;
y 81.3%; Pred. No. 7.
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                                                                                                                                                                                                                                    NA; 1107 BP.
associated C35
                                                                                                                                             22.1%;
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83.0%;
                                                                                                                                                                                                                                                                         22.1%;
81.3%;
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83.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256157 BP.
(CA) gene HD07-114
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Pred.
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Pred.
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Pred.
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Pred. No. 3.9e-46;
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                                                                                                        encoding
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No. 3.46
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No.
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No.
                                                                                                                                              200; DB 12;
No. 6.4e-47;
                                                                                                                                                                                                                                                                                                                                                                                                       200.2; DB 13;
No. 4.5e-46;
                                                                                                                                                                                                                                                                            200; DB 12;
No. 6.3e-47;
                                                                                                                                                                                                                                     promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.9e-46;
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Ω
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3.4e-46;
                                          . 7e
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                                             -6;
47;
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                                                      Length
                                                                                                                                                         Length 1107;
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Query Match
Best Local Similarity
RESULT 666
ID ARSoco
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RESULT 663
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Best Local Similarity
RESULT 664
                       Best Local Similarity RESULT 671
                                                                               Best Local Similarity
RESULT 670
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                                                                                                                                         Best Local Similarity
RESULT 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                            ADF90165 standard; DNA; 46649 BP.
Genomic DNA encoding human transporter protein.
Geny Match
22.1%; Score 200; DB 10;
set Local Similarity 79.1%; Pred. No. 2.7e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic DNA #176
US2002119919-A1.
29-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human colorectal cancer antigen coding WO200155350-A1. 02-AUG-2001.
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06-MAY-2004.
                                                                                                                                                                                                            ACC00503 standard; DNA; 23434 BP. Human histone deacetylase HDAC10 WO20030143340-A2.
                                                                                                                                                                                                                                                                                                           Human colorectal US2003054420-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human digestive system antigen WO200155314-A2.
                                                                                                                                                                            (NOVS ) NOVARTIS AG.
                                                                                                                                                                                                                                                                                                                                                                               (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.

ry Match 22.1%;

t Local Similarity 77.5%;
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ry Match 22.1%;
t Local Similarity 77.5%;
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ry Match 22.1%;
t Local Similarity 77.5%;
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ACN45002 standard; DNA; 60430 BP.
Human genomic sequence hCG33210.
                                                                     ADR03800 standard; DNA; 46649 BP
                                                                                                                                                                                                                                                                                                                                    ADB93125 standard; DNA;
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Genomic DNA #176 encoding human
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(ZAUD/) ZAUDERER M.
(PARI/) PARIS M.
                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                               20-MAR-2003
                                                                                                                                                                                                                                                                                                                       cancer
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78.1%;
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81.3%;
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77.5%;
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77.5%;
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                                                             transporter.
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No. 1.3e-46;
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No. 2.
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No. 1.
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No. 1
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No. 1.
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No. 1.
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No. 1.
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                                       DB 13;
.7e-46;
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-46;
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Best Local Similarity
RESULT 680
ID AAL37239 standard; I
DE Human musculoskeleta
PN W0200155367-A1.
PD 02-AUG-2001.
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Best Local Si
RESULT 674
ID ABD32806 E
DB Human canc
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RESULT 676
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                                                                                                                                                                                                                                                                                 JET LOVEL TO THE PROPERTY OF T
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02-SEP-2004.
(SAGR-) SAGRES DISCOVERY INC.
(SAGR-) 22.1%;
erv Match 22.1%;
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Osteoarthritis-associated polym
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cancer-associated WO2004074320-A2.
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                      Human musculoskeletal WO200155367-A1.
                                                                                                                                                                                                               Human colon cancer WO9958675-A2.
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(INCY-) INCYTE GENOMICS INC.
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PRINT 22.1%;
It Local Similarity 80.4%;
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Human cancer-associated genomic DNA HD16-059.
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(VITI-) VITIVITY INC.
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                                                                                                                                                 (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
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cell line
                                                                  DNA; 2306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.1%;
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85.4%;
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82
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polynucleotide
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No. 3.7e-46;
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No. 3.7e-46;
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No. 3e-46;
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                                         polymucleotide
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                                                                                                         .8; DB 3;
6.1e-47;
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4.8e-46;
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4.3e-46;
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                                                                                                                                                                                                                                                                                                   DB 11;
.5e-46;
                                                                                                                                                                                                                                     sequence
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                                            3604.
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Query Match
Best Local Similarity
RESULT 681

ID ABX60227 standard; c
DE CDNA encoding novel
PN US2002147140-A1.
PD 10-OCT-2002.
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                            Human musculoskeletal system-associated US2004009488-Al.
                                                                                    (ROSE/) ROSEN C A
(RUBE/) RUBEN S M
(BARA/) BARASH S (
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Human musculoskeletal sy
US2004009488-A1.
15-JAN-2004.
                                                                                                                        CDNA encoding novel US2002147140-A1.
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C
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                 (HUMA-) HUMAN GENOME
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DNA encoding novel signal
WO200154733-A1.
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WO2004048938-A2.
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EP1270724-A2.
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(HUMA-) HUMAN GENOME SCI INC.
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Human immune/haematopoietic antigen
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US2002168711-A1.
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(HUMA-) HUMAN GENOME
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                                                                         (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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Best Local Similarity
RESULT 698
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(HUMA-) HUMAN GENOME SCI INC.
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ery Match 22.0%;
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                                                                         ADQ97846 standard; DNA;
Human cancer associated
WO2004060304-A2.
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Human STAT5B gene.
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ry Match 22.0%;
t Local Similarity 81.1%;
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WO2003039484-A2.
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Human STAT5B gene genomic DNA
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Human FLAP genomic WO2004035741-A2.
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WO2003008583-A2.
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                    ADN06353 standard;
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PD 25-JAN-200
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29-APR-2004.
(DECO-) DECODE GENETICS EHF. (DECO-) Match
22.0%; (Sept Local Similarity 80.9%; (Sept Local Sim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cancer-associated (( W02004058146-A2.
                                                Human therapeutic contig W02004080148-A2. 23-SEP-2004.
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YEY Match 22.0%;
St Local Similarity 82.0%;
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(HYSE-) HYSEQ INC.
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(REGC) UNIV CALIFORNIA.
(22.0%;
St Local Similarity 76.7%;
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W02003073826-A2.
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ry Match 22.0%;
t Local Similarity 80.9%;
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Human soft tissue :
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10-JUN-2004.
(PROT-) PROTEIN DESIGN LABS INC.
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ry Match 22.0%; Score
t Local Similarity 84.6%; Pred.
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RESULT 723
ID ABK6°
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RESULT 722
ID AAI59666 standard; c
DE Human polynucleotide
PN W0200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
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RESULT 717
ID ADS11590 standard; D
DE Human therapeutic co
PN W02004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
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ID ADS111
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(NUVE-) NUVELO INC.
                          Human polynucleotide SEQ WO200153312-A1.
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                                                                                                DNA encoding human WO200224721-A1. 28-MAR-2002.
                                                                                                                                                            26-JUL-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                   ADI31927 standard; cDNA; 1748 BP
Full length human cDNA clone Seq
EP1396543-A2.
10-MAR-2004.
(REAS-) RES ASSOC BIOTECHNOLOGY.
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Human therapeutic contig DNA
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Novel human cDNA sequence
ABK83336 standard; cDNA; 4159 cDNA encoding human DPRP-2 spl W0200231134-A2.
                                                                                           ACN40423 standard;
Tumour-associated a
WO2004030615-A2.
                                                                                                                                                                                                                                                                                                                            ADQ86753 standard; cDNA; 4147 BP. Human tumour-associated antigenic WO2004060270-A2.
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13-JUN-2002.
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ry Match 22.0%; Score
Local Similarity 84.1%; Pred.
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cy Match 22.0%;
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        Human immune/haematopoietic an WO200157182-A2.
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Human therapeutic I
WO2004080148-A2
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RESULT 746
ID ABZ67767 standard; I
DE Human secreted prote
PN W0200277186-A2.
PD 03-OCT-2002.
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                                                                Human cancer-associated WO2004058146-A2.
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Human immune/haematopoietic an
WO200157182-A2.
09-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
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Human HPC2/ELAC2 gene
JP2004166565-A.
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                                    (SAGR-) SAGRES DISCOVERY

TY Match

L Local Similarity 78.6
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Human cancer-associated WO2004074320-A2.
                   ABD32612 standard; DNA;
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ry Match 22.0%;
t Local Similarity 82.9%;
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03-OCT-2002.
(HUMA-) HUMAN GENOME
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ry Match 22.0%;
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WATA/) WATANABE M.
FURU/) FURUSATO M.
HONS ) YAKULT HONSHA
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                                                                                                                       118788;
                                              135827;
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Que.
Best L.
RESULT 758
ID ABK92°
DE Hum?
PN WO'
PD 7
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RESULT 756
ID ADJ30214 standard; D
DE Human musculoskeleta
PN US200400948-A1.
PD 15-JAN-2004
PA (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
RESULT 752
ID ACM43374 standard, D
DE Human genomic sequen
PN W02003073826-A2.
PD 12-SEP-2003
PA (SAGR-) SAGRES DISCO
Best
RESULT
ID AA
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Best Local Similarity
RESULT 755
                                                                                             Best Local Similarity RESULT 759
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RESULT 757
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Best Local Similarity
RESULT 754
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Best Local Similarity
RESULT 753
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                                                                                                                                 Human prostate specific : MC200238810-A2.
16-MAY-2002.
                                                      Genomic sequence #330 encoding n W0200155301-A2.
                                                                                                                                                                                                                                 ADM03474 standard;
Human cDNA of the i
EP1347046-A1.
                                                                                                                                                                                                                                                                                                                   ADJ30214 standard; DNA; 1664 BP. Human musculoskeletal system-associated US2004009488-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human musculoskeletal system WO200155367-A1.
                                                                                                                                                                                                                                                                                                                                                                                                               cDNA encoding novel US2002147140-A1. 10-OCT-2002.
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Human inflammatory
WO200142511-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACN44374 standard; DNA; 181684 BP. Human genomic sequence hCG16651. WO2003073826-A2.
                                                                                                                                                                                       (REAS-) RES ASSOC BIOTECHNOLOGY.
ry Match 22.0%; Score
t Local Similarity 82.4%; Pred.
                                                                                                                                                                                                                       24-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ABX59464 standard;
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ry Match 22.0%;
t Local Similarity 83.1%;
                                          (HUMA-)
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (WHED ) WHITEHEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SAGR-) SAGRES DISCOVERY.
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                   Similarity
                                         HUMAN GENOME
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                                                                                                                            INC.
                                                                                                                                                                                                                                            invention SEQ :
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA; 1664
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                   SCI INC.
22.0%;
81.1%;
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22.0%;
86.4%;
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76.0%;
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86.4%;
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81.1%;
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related
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Pred. No.
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                    199.4;
No. 1.9
                                                                                                       199.4; DB 6;
No. 1.8e-46;
                                                                                                                                                                                         199.4; DB 1
No. 1.1e-46;
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No. 1.1e-46;
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No.
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No.
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                                                                        human
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1.1e-46;
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1.1e-46;
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5.4e-46;
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5.9e-46;
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                              DB
                                                                        enzyme
                              4.
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AAK69231 standard; DNA; 8658

ВP

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A (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity
RESULT 762
ID ACT.
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Best Local S
RESULT 764
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RESULT 761
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RESULT ADO
ID ADO
DE Hur
PN WO:
PD 22
PA (S:
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                                                                                                                                                                                                                                   RESULT 768
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Query Match 22.0%:
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Best Local
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Human transporter protein encoding
Pary Match
22.0%; Score
st Local Similarity 81.1%; Pred.
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Human transporter genomic DNA; Scor.
ary Match 22.0%; Scor.
it Local Similarity 81.1%; Pred
                                                                                                                                                                                            ADH19246 standard; DNA; 124165 BP.
Human 5-hydroxytryptamine receptor type
WC2003097873-A2.
                                                                                                                                                                                                                                                                                                                                                                                                 ADQ97870 standard; DNA; 121160 Human cancer associated sequenc WO2004060304-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACN44990 standard; DNA; 33317 BP Human genomic sequence hCG27461. WO2003073826-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAL53466 standard; DNA; 70372 BP
                                                                                                           ADF83402 standard; DNA; 124167 BP.
Human 5-hydroxytryptamine receptor type
Human 5-hydroxytryptamine receptor WO2003097873-A2.
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ry Match 22.0%;
t Local Similarity 81.3%;
                        ADH19240 standard; DNA;
                                                                                                NO2003100091-A1.
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                                                                        EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
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22.0%; Score 1
y 81.1%; Pred. 1
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81.1%;
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76.0%;
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| sequence H
                        124167 BP.
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Pred.
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Pred.
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e 199.4; DB 13;
. No. 4.1e-46;
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No.
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No.
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No. 4.7e-46;
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No. 3.5e-46;
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No.
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No. 2.1e-46;
           type
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No. 5.8e-46;
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2.2e-46;
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            38
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Query Match
Best Local Similarity
RESULT 771
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RESULT 774
ID ABD32598 standard;
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Best Local Similarity
RESULT 772
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Human transporter protein encoding
Human transporter 22.0%; Score
st Local Similarity 80.6%; Pred.
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                                                                                   AAK89418 standard; DNA; 28588 l
Human digestive system antigen
WO200155314-A2.
                                                                                                                                                                                                                                                                                                   (KETC/) KETCHUM K A. (DFRA/) DI FRANCESCO (BEAS/) BEASLEY E M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Osteoarthritis-associated polymorphic WO2003054166-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004060304-A2.
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                                                                                                                                                                                                                                    Human immune/haematopoietic WO200157182-A2.
                                                                                                                                                                                                                                                          AAK80126 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABD32598 standard; DNA;
Human cancer-associated
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TY Match 22.0%;

t Local Similarity 79.9%;
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ry Match 22.0%;
t Local Similarity 81.5%;
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Human liver ass
WO200155355-A1.
                    AAS31923 standard;
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                                                                 (HUMA-) HUMAN
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                                         ocal Similarity
         associated
                                                                 GENOME
                                                                                                                                                                                                                                                          DNA; 4115 BP
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                                         3 SCI INC
22.0%;
82.8%;
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81.1%;
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78.9%;
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76.7%;
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          genomic
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genomic DNA HD7-220.
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sequence HD08-028,
                       28588 BP
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e 199.2; DB 6;
. No. 3.4e-46;
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No. 1.8e-46;
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5.9e-46;
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8.1e-46;
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                                             ယည်
                                                                                                 sequence
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                                             .8e-46;
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RESULT 781
ID
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Best Local S
RESULT 785
ID ACN44230 i
DE Human gen
PN W020030731
PD 12-SEP-20
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Best Local S
RESULT 783
ID ABD33578
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RESULT 782
ID AREST
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RESULT 780
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RESULT 787
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RESULT 788
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22-JUL-2004.
(SAGR-) SAGRES DISCOVERY INC.
(SAGR-) SAGRES DISCOVERY INC.
22.0%;
ery Match 22.0%;
esry Match 82.8%;
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Human genomic sequence hCG1784975
W02003073BC-A2.
12-SEP-2003.
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Human lipase, hormone-sensitive (LIPE)
ary March
5t Local Similarity 83.0%; Pred. No.
                                                                                                           ADH56439 standard;
Human hypothetical
                                                                                                                                                                                                                         ADQ97968 standard; DNA; 78082 BP. Human cancer associated sequence WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                    ACN44230 standard; DNA; 66973 BP Human genomic sequence hCG21559. WO2003073826-A2.
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      ADC85301 standard;
Mouse Sos1 coding
WO2003045230-A2.
                                                                                   US2003232770-A1.
18-DEC-2003.
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"YE Local Similarity 80.6%;
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Human cancer-associated (CA) gene HD07-116
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ADJ15191 standard; DNA; 28588 BP.
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                                                                         (ISIS-) ISIS PHARM
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ry Match 22.0%;
t Local Similarity 84.4%;
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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                                                  Local Similarity
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                sequence
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                            DNA; 96591
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tumour endothelial marker DNA
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No. 6e-46;
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No. 5.8e-46;
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No. 4.5e-46;
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No. 3.8e-46;
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9.2; DB 6; Leng
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5.2e-46;
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5.1e-46;
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Query Match
Best Local Similarity
RESULT 798
ID ABA20857 standard; D
B Human nervous system
PN WO200159063-A2.
                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
RESULT 794
ID AAH11291 standard; cl
DE Human cDNA clone (3'.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INS
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Query Match 22.0%;
Best Local Similarity 76.0%;
RESULT 790
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Best Local Similarity
RESULT 795
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RESULT 797
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EP1074617-A2.
07-FFB-200
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Human SOS1 gene.
WO2003008583-A2.
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21.9%;
PY Match 21.9%;
Local Similarity 83.8%;
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Human carcinoma associated
US2004072154-A1.
15-APR-2004.
                                                                                                  ADQ64845 standard; cDNA; 4634 BP.
Novel human cDNA sequence #2006.
                                                                                                                                                                                 WO200157182-A2.
                                                                                                                                                                                            AAK70822 standard; DNA; 3371 BP.
Human immune/haematopoietic antigen
                                                                                                                                                                                                                                                                          WO200157182-A2.
  Human nervous system WO200159063-A2.
                                                                    (REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                        EP1440981-A2.
                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
ry Match 21.9%;
t Local Similarity 78.0%;
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ry Match 21.9%;
t Local Similarity 85.1%;
                                                                                                                                                                                                                                                                                   Human immune/haematopoietic
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(ENGE/) ENGELHARD E
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           DNA; 11234 BP.
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ID AAD482
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O9-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) EXP 21.9%;
ery Match 21.9%;
ery Match 80.1%;
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(GONG/) GONG F.
(DFRA/) DI FRANCESCO V.
(BEAS/) BEASLEY E M.
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ary Match 21.9%; Score 199; DB 6;
t Local Similarity 85.1%; Pred. No. 4.5e-46;
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Human transporter protein DNA
L1.9%; Scor
St Local Similarity 85.1%; Pred
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(HUMA-) HUMAN GENOME
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                                                                                                                                                                                                                                                                                          ABD32585 standard; DNA; 50927 BP. Human cancer-associated genomic DNA WO2004074320-A2.
                                                                                                                                                                                                                                                                                                                                                                     Human enzyme protein
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                                                          ACN44602 standard; DNA; 126266 BP.
Human genomic sequence hCG1781402
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(HUMA-) HUMAN GENOME
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CY Match 21.9%;
Local Similarity 85.1%;
                        SAGR-) SAGRES DISCOVERY
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h 21.9%;
Similarity 85.1%;
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21.9%;
80.1%;
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21.9%;
81.3%;
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21.9%; Score 199;
85.1%; Pred. No. 4
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81.5%;
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Pred. No. 4.7e-46;
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Pred. No. 4
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No. 4.
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No. 7.
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No. 4.
199; DB 11;
No. 7.6e-46;
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No. 5.4e-46;
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.5e-46;
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.1e-46;
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.7e-46;
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.2e-46;
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RESULT 809
ID ADH630
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RESULT 810
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Best Local Similarity
RESULT 819
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Human NUMA1/FLJ20625/LOC220074 rec
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                                                                                         Human MDR1 related WO2003013535-A2.
                                                                                                                                                                         Human MDR1 related WO2003013537-A2. 20-FEB-2003.
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Human fibroblast growth
Human genomic sequence hCG39530
WO2003073826-A2.
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WO2003013536-A2.
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                       ACN44170 standard;
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                                              (BPID-) EPIDAUROS BIOTECHNOLOGIE AG. ry Match 21.9%; Score 1 t Local Similarity 82.6%; Pred. N
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h 21.9%; Score 1
Similarity 82.6%; Pred. N
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h 21.9%; Score 199;
Similarity 82.6%; Pred. No. 8
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related nucleic acid
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21.9%;
81.5%;
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DNA sequence
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DNA sequence SE
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sequence SEQ
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21.9%; Score 199; DB 10; Length 1
79.3%; Pred. No. 8.1e-46;
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core 199; DB 12;
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ID NO:669.
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RESULT 820
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(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
21.9%; Score 199; DB 10;
ery Match 21.9%; Pred. No. 1.1e-45;
                                                                                                                                                                                                                                                     ADR14082 standard; DNA; 2591 BP. Human NF-kappaB pathway-associated WO2004065577-A2.
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                                                                                             Human periodontal
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(REAS-) RES ASSOC BIOTECHNOLOGY.
ry Match
21.9%; Score
27.0001 Similarity 85.9%; Pred.
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BP1447413-A2.
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07-FEB-2001.
(HELI-) HELIX RES
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Human cDNA sequence SEQ ID NO:15042.
            AAK81266 standard;
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                                                                                                      ACN37218 standard;
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ry Match 21.9%;
t Local Similarity 75.2%;
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Human cancer related polynucleotide SEQ
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ry Match 21.9%;
Local Similarity 81.8%;
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                                                  (HUBI-) HUBIT GENOMIX INC. (KAMO/) KAMOI K.
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(HYSE-) HYSEQ INC.
                               Local Similarity
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266 standard; DNA; 21458 BP. immune/haematopoietic antigen
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y 81.
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) ID NO:1369.
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Query
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Best Local Similarity

RESULT 833

ID ADADOTTO
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Best Local S
RESULT 832
                                      Best Loc
RESULT 837
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Best Local Similarity
RESULT 830
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RESULT 829
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      ACN37244 standard;
Human periodontal d
ery Match
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                                                                                         Human HNFlalpha gene WO2004016813-A2.
                                                                                                                                                                           Human hCG1745228 gene WO2003039484-A2.
                                                                                                                                                                                    ADE95950 standard; DNA; 21666
Human hCG1745228 gene genomic
                                                                                                                                                                                                                                                             Human CA gene.
WO2003008583-A2.
                                                                                                                                                                                                                                                                                                                                              Human Nuprl carcinoma associated WO2003057146-A2.
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                                                                                                   ADK40307 standard; DNA; 23469 BP.
Human HNF1alpha gene SEQ ID NO:27.
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02-AUG-2001.
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                                                                                                                                                                                                                                                                       Human CA
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ry Match 21.9%;
c Local Similarity 84.9%;
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ry Match 21.9%;
t Local Similarity 83.0%;
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th 21.9%;
Similarity 84.9%;
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ch 21.9%;
Similarity 84.9%;
l disease related (
21.9%; Score
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antigen encoding
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system related
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21.9%; S
77.3%; P
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Score 198.8; DB 12;
Pred. No. 4.6e-46;
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g novel human
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No. 4.4e-46;
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No. 4.4e-46;
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        IL4R SEQ ID .8; DB 13;
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4.4e-46;
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4.4e-46;
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4.4e-46;
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Score 198

NO:154. Length 25382;

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Best Local Similarity
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Human genomic sequence hCG17357.
WO2003073826-A2.
12-SEP-2003.
12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
LOCAL Similarity 82.1%; Pred.
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(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
21.9%;
ery Match 21.9%;
ery Match 81.2%;
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15-JUL-2004.
(SAGR-) SAGRES DISCOVERY INC.
21.9%;
xy Match 21-9%;
86.2%;
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WO200104270-A1.
                                                                                     ADL13479 standard; DNA; 84539 BP.
Osteoarthritis-associated polymorphic
WO2003054166-A2.
                                                                                                                                                                                       Stomach cancer related gene sequence WO200194629-A2.
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 ADM29048 standard;
Human interleukin '
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                                    (INCY-) INCYTE GENOMICS INC.
TY Match 21.9%;
Local Similarity 75.6%;
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DNA; 130020 BP.
4 receptor (IL4F
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Pred. No. 5.8e-46;
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Pred. No. 5.7e-46;
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Pred. No. 4.9e-46;
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No. 5.7e-46;
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No. 7.5e-46;
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No. 6.2e-46;
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No.
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RESULT 853
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WO200177291-A2.
18-OCT-2001.
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                                                                                                                                                                                  (ZHOU/) ZHOU P.
(TANG/) TANG Y T.
(LIUC/) LIU C.
(ASUN/) ASUNDI V.
                                                                                                                                                                                                                                                                                                                                                                                            Human polynucleotide SEQ WO200153312-A1.
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        AAK68667 standard; DNA; 4963 BP.
Human immune/haematopoietic antigen
WO200157182-A2.
09-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                          AAK83412 standard; DNA; 4156 Human immune/haematopoietic aw0200157182-A2.
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"Y Match 21.9%;

It Local Similarity 83.3%;
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07-APR-2004.
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                                                                                                                                                                       (DRMA/) DRMANAC R
                                                                                                                                                                                                                                     Novel human cDNA
US2003104529-A1.
                                                                                                                                                                                                                                              ADB48552 standard;
Novel human cDNA SI
                                                                                                                                                                                                                                                                                                                    DNA encoding human US6569662-B1.
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ry Match 21.9%;
t Local Similarity 82.1%;
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                                                                                          (HUMA-) HUMAN GENOME
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h 21.9%;
Similarity 85.4%;
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GPCR-like p
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21.9%;
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21.9%;
80.3%;
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21.9%; Score 198.8;
82.1%; Pred. No. 8.9
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NO 462.
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No.
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-46;
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RESULT 859
ID ADROF
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RESULT 858
ID ADJ30276 standard; D
DE Human musculoskeleta
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME
                                                                           Best Local Similarity
RESULT 863
ID ABA94501 standard; E
DE Human proto-oncogene
PN US6340584-B1.
PD 22-JAN-2002.
                                 Query Match
Best Local S
RESULT 864
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RESULT 861
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(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
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ery Match 21.7%;
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(HUMA-) HUMAN GENOME SCI INC.
21.9%;
ery Match
21.9%;
80.3%;
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                                                                                                  ABA94501 standard; DNA; 15297
Human proto-oncogene tyrosine
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EP1447413-A2.
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Human musculoskeletal system-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA encoding novel
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Human kinase genomic WO200277191-A2.
                      ABV75414 standard;
                                                                  (PEKE ) PE CORP NY
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                                                                                                                                                                                        ABK84514 standard; cDNA; 12263 BP.
Human cDNA differentially expresse
                                                                                                                                                                                                                                                  (BARA/) BARASH S C
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Human novel polynucleotide #943.
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                           (GENE-) GENE LOGIC
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RUBE/) RUBEN S M.
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human cDNA useful
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21.9%;
80.8%;
                      DNA; 15297 BP.
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No. 4.4e-46;
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3e-46;
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Best Loc
RESULT 870
ID ADQ977
DE Hump
PN WO'
PD 90 7
PA
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RESULT 872
ID AAK68725 standard; Di
DE Human immune/haemato;
PN WO200157182-A2.
PD 09-AUG-2001.
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RESULT 866
ID AAK75677 standard, D.
DE Human immune/haemato.
PM w0200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME
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Best Local Similarity
RESULT 865
ID ADM28582 standard; c
DE Human proto-oncogene
PN US2004063130-A1.
PD 01-APR-2004.
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ID ABA081
DE Human
PN WO2001
PD 02-AUG
PA (HUMA-
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ID AAK684
DE Human
PN WO2001
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17-APR-2003.
(GENO-) GENOME THERAPEUTICS (GENO-)
ery Match 21.9%;
ery Match 82.8%;
                                                                                                                                                                                                                                                                  Human cancer associated w02004060304-A2.
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ABQ76896 standard; DNA; 53226 BP. Human G-protein coupled receptor US2002142951-A1.
                                                                                                           AAK68725 standard; DNA; 47090 BP. Human immune/haematopoietic antigen
                                                                                                                                                                                     Human immune/haematopoietic WO200157182-A2.
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(PEKE) PE (
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(HUMA-) HUMAN GENOME
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ry Match 21.9%;
t Local Similarity 82.8%;
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fragment #4.
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No. 4.5e-46;
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Best Local Similarity
RESULT 878
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Best Local Similarity
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Osteoarthritis-associated
WO2003054166-A2.
                                                                                                                                                                                                                                          10-JUN-2004.
10-JUN-2004.
(PROT-) PROTEIN DESIGN LABS INC.
(PROT-) PROTEIN DESIGN LABS INC.
21.9%; Sco
22.7%; Pre
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(ISIS-) ISIS PHARM INC.
21: xy Match
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                                                                                                                       ACN44930 standard; DNA; 106378 BP Human genomic sequence hCG1742422 WO2003073826-A2.
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(BEAS/)
(KETC/)
                                                                                                                                                                                                                                                                                       Human soft tissue sarcoma-upregulated WO2004048938-A2.
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Human osteoblast differentiation related
                                                                                                                                                                                                                                                                                                            ADQ18878 standard; DNA; 86080 BP.
                                         WO2004039954-A2.
                                                   ADO32260 standard; DNA; 106707 BP.
Human chromosome 20 region containing
                                                                                                                                                              (INCY-) INCYTE GENOMICS INC

TY Match 21.9%;

Local Similarity 82.7%;
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                                                                                                     SAGR-) SAGRES DISCOVERY.
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) BEASLEY E M.
) KETCHUM K A.
) DI FRANCESCO
JOSLIN DIABETES CENT
h 21.9%;
Similarity 82.8%;
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Pred. No. 8.6e-46;
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is a
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No. 8.
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No. 7.1e-46;
                                                                                  198.6; DB 1
No. 9.3e-46;
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8.6e-46;
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   .6; DB 12;
9.3e-46;
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Query Match
Best Local S
RESULT 883
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                  Best Local Similarity RESULT 892
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ry Match 21.9%;
t Local Similarity 82.8%;
                                                                                                                                        Colon adenocarcinoma WO200194629-A2.
                                                                                                                                                                                                                                                                                                                 ABL66806 standard; DNA; 145831
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                                                                                  ABT10149 standard; cDNA; 145831 BP
                                                                                                                                                           ABL62309 standard;
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        AAH92378 standard;
                                              (GENE-) GENE LOGIC
                                                                 WO200259271-A2.
                                                                          Human breast cancer associated coding
                                                                                                                                                                                                (AVAL-) AVALON PHARM
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duman inflammatory
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associated
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                         ' INC.
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r associated coding
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bowel dis
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na related gene
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No. 9.8
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No.
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No.
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No. 9.4e-46;
                                                                                                                                                                               198.6; DB 6;
No. 1.1e-45;
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No.
                             198.6; DB 6;
No. 1.1e-45;
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.8e-46;
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.9e-46;
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gene
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PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SI
QUETY MATCH 2:
Best Local Similarity 8:
RESULT 894
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RESULT 893
ID ABK42296 standard; E
DE Genomic sequence #19
PN WC200155343-A1.
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
RESULT 898
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RESULT 895
                                                           Query Match
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(HUMA-) HUMAN GENOME SCI INC.
21.9%;
21.9%;
27.2%;
ABK86229 standard; DNA;
AIP-1/FLASH promoter rel
WO200255691-A1.
                                                                                                            ABK86220 standard; DNA; 13919 BP.
AIP-1/FLASH promoter related DNA sequence
                                                                                                                                                                                                AIP-1/FLASH promoter WO200255691-A1.
                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence WO9727284-A2.
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(REAS-) RES ASSOC BIOTECHNOLOGY.
21.9%; Score
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Human cDNA of the
EP1347046-A1.
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Genomic sequence #195 encoding novel human connective tissue polypeptide.
W0200155343-A1.
                                                                      18-JUL-2002.
(NIPK ) NIPPON KAYAKU
                                                                                                 WO200255691-A1.
                                                                                                                                                                                                                           ABK86221 standard;
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(GENE-) GENELABS TECHNOLOGIES INC.

(GENE-) $21.9%; Score

ry Match 21.9%; Pred.
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Nucleotide sequence encoding
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ry Match 21.9%;
t Local Similarity 78.8%;
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(BLLI-) ELLIPSIS BIOTHERAPBUTICS CORP.
21.9%; Score 198.4;
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21.9%;
81.0%;
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78.8%;
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78.8%;
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No. 2.5e-46;
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                                                198.4; DB 6
No. 4.9e-46;
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No. 4.9e-46;
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No. 3e-46;
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No. 2.2e-46;
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No. 2.2e-46;
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. 1.5e-46;
                                                                                                                                                 3.4; DB 6;
4.9e-46;
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Query Match
Best Local S
RESULT 905
ID AAK89230
                     Best Loca
RESULT 910
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Best Local Similarity
RESULT 902
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                                                                                                                               Query Match
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                                                                         Human genomic sequence WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADQ97189 standard; DNA; Human cancer associated WO2004060304-A2.
ADP13458 standard; DNA; 87869 BP.
Renal cell carcinoma differentially expressed gene
                                                                                                                                                               Human periodontal WO2004042054-A1. 21-MAY-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAK89230 standard; DNA; 30110 BP. Human digestive system antigen ge W0200155314-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADS36465 standard; DNA; 25322 BP.
Human autoimmune disease-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADR66994 standard; DNA; Human cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUL-2002.
(NIPK ) NIPPON KAYAKU
                                                                                                ACN45166 standard; DNA;
                                                                                                                                                                                                                                                                          Human WKL-1 g
EP1209229-A1.
                                                                                                                                                                                                                                                                                                                                                                         ADS36492 standard; DNA; 34059 BP Human autoimmune disease-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004074321-A2.
02-SEP-2004.
                                                                                                                                          (KAMO/) KAMOI
                                                                                                                                                                                                ACN37238 standard; DNA; 48753
                                                                                                                                                                                                                                          (MEYE/) MEYER
                                                                                                                                                                                                                                                                                               AAD31198 standard;
                                                                                                                                                                                                                                                                                                                                                               WO2004083403-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004083403-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SAGR-) SAGRES DISCOVERY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (APPL-) APPLERA CORP.
                                                                                                                                                                                                                                                                                                                                        APPL-) APPLERA CORP.
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                               Local Similarity
                                                     SAGRES DISCOVERY.
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                                                                                                                                                                                                                                                                                    genomic
                                                                                                                                          GENOMIX INC.
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                                                                                                                                                                                      disease
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                               21.9%;
83.0%;
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78.8%;
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79.9%;
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78.8%;
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hCG37872.
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sequence
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related
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Pred. No. 6.9
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                                 198
No.
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No. 6.5
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No. 6.9e-46;
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No.
                                                                                                                      198.4; DB 13;
No. 7.9e-46;
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No. 6.1e-46;
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No.
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6.9e-46;
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6.5e-46;
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.9e-46;
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Best Local Similarity
RESULT 913
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                                                                                                                                                           Query Match
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03-UTL-2003.
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Human IDE gene variant DNA sequence SeqID187.
US2003224380-A1.
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                                                                                                                                                                                                Ovary cancer related WO200194629-A2.
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(GEHO) GEN HOSPITAL CORP.
ry Match 21.9%;
t Local Similarity 79.6%;
                                                                                                           Human soft tissue sarcoma-upregulated
                                                                                                                                                                                                                                                                                                                                                                                                                              ABK83573 standard; cDNA; 130263 BP.
Human cDNA differentially expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SAGR-) SAGRES DISCOVERY.
(SAGR-) SAGRES DISCOVERY.
(SAGR-) SAGRES DISCOVERY.
21.9%;
Local Similarity 81.4%;
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          ABX16034 standard; DNA; 203654 BP.
Human gene encoding calcium channe
                                                                                                WO2004048938-A2.
                                                                                                                                                                                                                       ABL68122 standard; DNA; 174424 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                #0200228999-A2.
Human gene encoding 
US2002142938-A1.
                                             (PROT-) PROTEIN DESIGN LABS INC.
ry Match 21.9%; Sco
t Local Similarity 84.8%; Pre
                                                                                                                        ADQ19573 standard; DNA; 181343 BP
                                                                                                                                                                                                                                                                                                                            Genomic sequence encoding a human NgR2 protein
                                                                                                                                                                         (AVAL-) AVALON PHARM.
                                                                                                                                                                                                                                                                          (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                O200229059-A2
                                                                                                                                                                                                                                                                                                                                      AL38336 standard; DNA; 143899 BP.
                                                                                                                                                                                                                                                                                                                                                                                        GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEHO ) GEN HOSPITAL CORP.
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) STOVER J A.
) SLONI D K.
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BURCZYNSKI M
TREPICCHIO W
                                                                                                                                                21.9%;
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81.0%;
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81.0%;
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79.6%;
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Pred. No. 1.:
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Pred. No. 9.9e-46;
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No. 1.2
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No.
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No. 1.:
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No. 1.2e-45;
                                                198.4; DB 12;
No. 1.3e-45;
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          transporter family member.
                                                                                                               DNA
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1.1e-45;
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1e-
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                                                                                                                                                  ; DB 6;
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Best Local Similarity RESULT 919
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 PA PA
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24-SEP-2003.
(REAS-) RES ASSOC BIOTECHNOLOGY.
21.9%; Score
ery Match 72.7%; Pred.
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(YANC/) YAN C
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADO15750 standard;
4 synthesis-period
WO2004039975-A1.
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(PROG-) PROGENTIOR INC.
21.9%;
21.9%;
22.2%;
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Pry Match 21.9%;
It Local Similarity 79.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAK66647 standard; DNA; 598 BP.
Human immune/haematopoletic antigen
WO2001571B8-A2.
09-AUG-2001.
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(DFRA/) DI FRANCESCO
(BEAS/) BEASLEY E M.
(MAOM/) MAO M.
(DAIH/) DAI H.
(HEYY/) HE Y.
                                                     ADH28814 standard; DNA;
Human chronic myclogenou
US2003104426-Al.
                                                                                                                                                  Human lung cancer associated WO200224057-A2.
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18-OCT-2001.
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ry Match 21.9%;
t Local Similarity 81.7%;
                                                                                                                                                                         ABK70289 standard; cDNA; 4824
                                                                                                                                                                                                                                                                                                                                                      Human cDNA of the
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                                                                                                                           (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                            (HISM ) HISAMITSU PHARM CO LTD.
                                                                                                                                                                                                                         GENETICS INST INC.
                                    LINSLEY
                                                                     myclogenous
                                                                                                                                                                                                                                                                                                                                                     ; cDNA; 2062 BP invention SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA; 1714 BP. of neuroblastoma
                                                                                                                                                                                                                                                                                                                                                                                         21.9%;
80.5%;
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82.9%;
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72.7%;
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Pred. No. 1.4
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Pred. No. 1.4e-45;
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Pred.
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protein,
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No.
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No. 2.7e-46;
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No.
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. 2.5e-46;
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1.7e-46;
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2.9e-46;
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                                                                                                        .2; DB 6;
3.7e-46;
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Best Local Similarity
RESULT 935
ID AAL04340 standard; D
DB Human reproductive s
PN W0200155320-A2.
PD 02-AUG-2001
PA (HUMA-) HUMAN GENOME
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RESULT 928
ID ABOAGE
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RESULT
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Best Local Similarity
RESULT 932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 929
                                                                                    Query Match
                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                    AAS17764 standard; DNA; 24843 BP
Human Genomic DNA for CRYBB1.
WO200185998-A1.
                                                                                                                                                                                                                                                                                                                  AAK74096 standard; DNA; 21777 BP. Human immune/haematopoietic antigen W0200157182-A2.
                                                                                                            WO2004074321-A2.
02-SEP-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADR06591 standard;
Full length human of
EP1447413-A2.
                                                                       (SAGR-) SAGRES DISCOVERY INC.
ry Match 21.9%;
t Local Similarity 77.4%;
                                                                                                                                                                 020018557.

.5-NOV-2001.

(GENA-) GENAISSANCE PHARM INC.

(GENA-) GENAISSANCE PHARM INC.

21.9%; Score

81.7%; Pred.
                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                    WO200212497-A2.
14-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                             Human NFKBIB gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD32327 standard;
Human NFKBIB gene,
WO200212497-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAK80970 standard; DNA; 6159 BP.
Human immune/haematopoietic antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS44656 standard;
Human full-length;
WO200164834-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REAS-) RES ASSOC BIOTECHNOLOGY.
xy Match 21.9%; Score
t Local Similarity 81.3%; Pred.
                                                                                                                                               ADR67086 standard; DNA; 29328 BP
                                                                                                                                                                                                                                                                                                                                                                 (GENA-) GENAISSANCE PHARM INC.
ry Match 21.9%; st
t Local Similarity 79.2%; f
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD32179 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RADI/) RADICH J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENA-) GENAISSANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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  HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                andard; cDNA; 4865 BP.
human cDNA useful for treating neurological
                                                                                                                                 associated gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; DNA; 4885 BP. polynucleotide sequence
                                     DNA; 32194 BP.
system related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA; 15765 BP. alternative ve
                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA; 15765 BP
                                                                                                                                                                                                                                                                   21.9%;
80.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 SCI INC.
21.9%;
80.8%;
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79.2%;
   SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.9%;
72.7%;
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72.7%;
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Pred.
                                                                                                                                 genomic sequence
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                                     antigen
                                                                       198.
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No.
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No.
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No. 5.8e-46;
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                                                                                                                                                                                                                                                                                                                                                                  198.2; DB 6;
No. 5.8e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198.2; DB 4
No. 4.1e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198.2; DB 4;
No. 3.7e-46;
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No. 3.7e-46;
                                                                                                                                                                                                                                                                                                                              genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic
                                                                       7.4e-46;
                                                                                                                                                                      .2; DB 6;
6.9e-46;
                                                                                                                                                                                                                                                                    .2; DB 4;
6.6e-46;
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3.7e-46;
                                      DNA
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                                                                                                                                                                                                                                                                                                                               sequence
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                                     SEQ
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                                     ö
                                                                                                                                    NO:132
                                                                                                                                                                                                                                                                                                                               SEQ ID
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ARCUSSC

AREI/) FREIER S M.

AUGY MATCH

Best Local Similarity

RESULT 937

ID AD0726093 stand-
DE Human PIPST

PN US20037

PD 18-7

PA
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Best Local Similarity
RESULT 936
ID ADS19371 stan*
DE Human PIP'
PN US20**
                                                                                                                                                                       RESULT 941
ID ADD0252
DE Human
PN W02004
PD 21-MAY
PA (SACK/
PA (CREN/
PA (MIRR/
PA (MIRR/
PA (SHAO/
                                                          Best Local Similarity RESULT 943
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Best Local Similarity
RESULT 942
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Best Local Similarity
RESULT 939
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                                                                                                  Nucleotide sequence FR2798138-A1.
                                                                                                                      AAF84800 standard; DNA; 110000 BP Nucleotide sequence of the human (
                                                                                                                                                                                                                                                                                                               Human cancer-associated genomic DNA HD16-028 WC2004074330-A2.
                                                                                                                                                                                                                                                                                                                                                                              ADB16927 standard; DNA; 49806 BP.
Human DYXC1 DNA, chromosomal gene
WO2003068814-A1.
21-AUG-2003.
(LICN ) LICENTIA LTD.
WO200299122-A1.
        ACD13448 standard; DNA; 115756 BP. Human DNA encoding a p53 modifier,
                                                                                                                                                                                                                                                                                                            02-SEP-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genomic sequence WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACN45050 standard; DNA;
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                                                                                                                                                                                                                                     Human protein kinase
WO2004041212-A2.
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                                                                                                                                                                                             (HERN/)
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                                                                                                                                                                                             ) SACKTOR T C.
) CRARY J F.
) HERNANDEZ A I.
                                                                                                                                                                         MIRRA S.
SHAO C.
                                                                                                                                                                          SHAO
                                                                                        CNRS
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                                       Similarity
                                                                   S CENT NAT RECH S
21.9%;
ilarity 80.5%;
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21.9%;
75.9%;
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genomic DNA
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80.5%;
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82.9%;
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79.4%;
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82.7%;
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82.9%;
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75.9%;
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iota/lambda
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a related
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Score
Pred.
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Pred. No. 7.7e-46;
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                                                                                                                       SPG4
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                                       198.2;
No. 1.2
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No. 8.2
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No. 1.1e-45;
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No. 9.9e-46;
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No. 8.5e-46;
          SEQ.
                                                                    198.2; DB 5
No. 1.2e-45;
                                                                                                                                                                                                                                               genomic
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. 9.1e-46;
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8.2e-46;
                                        1.2e-45;
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          89
                                                 DB 6;
                                                                                                                                                              DB 12;
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                                                Length 110000;
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Best Loca
RESULT 947
ID ADQ594
Best
RESULT
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PN WO
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PD 07
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RESULT 951
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RESULT 949
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                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JAN-2003.

(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

(ADAC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

21.9%; Score 198.2; DB 10;

11. Local Similarity 75.5%; Pred. No. 1.9e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC87010 standard; DNA; 349999
Human GPCR gene SEQ ID NO:1463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SAGR-) SAGRES DISCOVERY INC. (SAGR-) SAGRES DISCOVERY INC. 21.9%; ry Match 21.9%; 78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hereditary haemochromatosis WO9814466-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV57903 standard; DNA; 237326 BP.
                                                                                                                            AAK76477 standard; DNA; 9409
Human immune/haematopoietic a
                                                                                                                                                                                                                                                                                                                Human cDNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-APR-1998.
(PROG-) PROGENTIOR INC.
                                    AAD34213 standard; DNA; 9432 BP.
Human cytochrome P450 2D6 (CYP2D6)
                                                                                                                                                                                    09-AUG-2001.
(HUMA-) HUMAN GENOME
                                                                                                                                                                                                             WO200157182-A2.
                                                                                                                                                                                                                       Human immune/haematopoietic antigen genomic sequence
                                                                                                                                                                                                                                                                                                        EP1347046-A1.
                                                                                                                                                                                                                                                                                                                                                   (PROT-) PROTEIN DESIGN LABS INC.
ry Match 21.8%; Sco
t Local Similarity 78.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                 Human soft tissue
WO2004048938-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ISIS-) ISIS PHARM
                                                                                                                                                                                                                                  AK68971 standard; DNA; 7770 BP.
                                                                                                                                                                                                                                                                                24-SEP-2003.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                        ADQ24208 standard;
                                                                                                                                                                                                                                                                                                                               NDM01910 standard;
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                                                                    A-) HUMAN GENOME SCI INC. latch 21.8%; cal Similarity 81.2%;
                                                                                                                                                                                                                                                                                                                   l, cDNA, 246
invention
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21.9%;
V 81.9%;
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sarcoma-upregulated
                                                                                                                                                              3 SCI INC.
21.8%; 1
83.6%; 1
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81.6%;
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82.9%;
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85
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d oncogene-3
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ion SEQ ID NO:595.
                                                                                                                             9 BP.
antigen
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Pred.
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Pred. No. 3e-46;
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Pred.
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Pred.
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Pred. No. 5.
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No.
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No.
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No. 3.3e-46;
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No. 1.7e-45;
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                                                                       198;
                                                                                                                            genomic
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1.3e-45;
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.le-46;
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Human ovarian and breast cancer a
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(BARA/) BARASH S C.
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Novel human DNA repair protein,
US2002086353-A1.
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                                                           Human reproductive WO200155320-A2.
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(BARA/) BARASH S C.
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RESULT 976
ID ACN44918 standard; Di
DE Human genomic sequen.
PN W02003073826-A2.
PD 12-SEP-2003.
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ID ABX611
DE Genom
PN US200:
PD 03-OC
PA (GONG
PA (KETC,
PA (DFRA,
PA (BEAS,
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Best Local Similarity
RESULT 975
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Best Local Similarity
RESULT 974
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                                                                                                                                                                                                                                                            ADA02684 standard; DNA; 59817 BP. Human DUSP10 carcinoma associated
                                                                                                                                                                                                                                                                                                                                     ACN44918 standard; DNA; 55114 BP. Human genomic sequence hCG20493. WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomic DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic DNA encoding US2002142381-A1. 03-OCT-2002.
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                                                                             Human DUSP10 gene WO2003039484-A2.
                                                                                       ADE95932 standard; DNA; 59817 Human DUSP10 gene genomic DNA
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                                                                                                                     (SAGR-) SAGRES DISCOVERY.
ry Match 21.8%;
t Local Similarity 82.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADA49717 standard; DNA; 40645 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KETC/) KETCHUM K A.
(DFRA/) DI FRANCESCO
(BEAS/) BEASLEY E M.
    AAD42934 standard; DNA; 70000 E
Human phospholipase A2 (PLA2),
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                                                                                                                                                                                                                                                                                           (SAGR-) SAGRES DISCOVERY.
ry Match 21.8%;
t Local Similarity 82.4%;
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                                   Local Similarity
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                                  3 DISCOVERY.
21.8%;
arity 82.6%;
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21.8%;
82.4%;
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82.6%;
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83.5%;
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21.8%; Score 198; DB 9;
76.7%; Pred. No. 9.6e-46;
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No. 1.1e-
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No. 1.1e-
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No. 1.1e-45;
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No. 8.
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1.1e-45;
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9.6e-46;
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      (Ca2+-independent)
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Query Match
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RESULT 982
ID AALS
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RESULT 981
ID ACN44938 standard; D
DE Human genomic sequen
PN W02003073826-A2.
PD 12-SEP-2003.
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RESULT 983
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RESULT 987
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RESULT
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12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
21.8%;
21.8%;
21.8%;
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WO2003073826-A2.
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25-JUN-2002.
(ISIS-) ISIS PHARM
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(PROTE) 21.8%; SCOTE
21.8%; Pred.
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WO2004048938-A2.
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                                                                                              ABK84797 standard; cDNA; 149671 BP. Human cDNA differentially expressed WO200228999-A2.
                                                                                                                                                                                 Human fibroblast
WO2003024987-A1.
                                                                                                                                                                                                                                                                     Human cancer associated sequence WO2004060304-A2
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          ADB70361 standard;
Moesin cDNA SEQ ID
WO2003021229-A2.
                                                                                                                                                                                            ADH63063 standard; DNA; 132762 BP.
Human fibroblast growth factor receptor
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ry Match 21.8%; Score
t Local Similarity 78.8%; Pred.
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                                                                         (GENE-) GENE LOGIC
                                                                                                                                                            (ISIS-) ISIS PHARM INC.
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ry Match 21.8%;
t Local Similarity 76.0%;
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sarcoma-upregulated
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                      cDNA; 149671 BP
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No. 1.4e-45;
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No. 1
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No. 1.4e-45;
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No. 1.4e-45;
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.2e-45;
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JOHM ) BRIGHAM & JUETY MATCH
Best Local Similarity
RESULT 991
ID ADJ37140 stand DE Human mali PN US2003 PD 27 PD 27 PA
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RESULT 993
ID ADPIACE
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Osteoarthritis-associated
WO2003054166-A2.
                                                                                                                                                                                                                                                   Human polynucleotide SEQ ID NO W0200153312-A1.
                                                                                                                                                                                                                                                                                                 18-OCT-2001.
(GEMY) GENETICS INST INC.
21.8%;
EXY Match
21.8%;
70.0%;
70.0%;
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                                                                                                                                                                                                                                                                                                                                         ABK35888 standard;
cDNA sequence #279
WC200177289-A2.
                                                                                     Genomic DNA for Human GABAB WO9921890-A1. 06-MAY-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein gene WO200056882-A1.
                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADF14037 standard; DNA; 1167 BP.
Human endometrial-specific DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INCY-) INCYTE GENOMICS INC.
                 Human reproductive WO200155320-A2.
                                                                                                                    AAX58061 standard; DNA; 16707
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                                                                                                                                                           (HYSE-) HYSEQ
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                                       AAL03377 standard;
                                                                             (ASTR ) ASTRA AB.
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HUMA-) HUMAN GENOME
                                                          Local Similarity
                                                                                                                                                           INC.
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pleural mesothelioma (MPM)
                           DNA; 21913
system relai
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tein gene 37
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Hest Loca
Best Loca
RESULT 1001
ID AALA
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RESULT 1003
ID ADTAINST
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RESULT 1000
ID AMIGNATION
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Best Local S
RESULT 1004
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Best Local Similarity
RESULT 1008
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RESULT 1007
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RESULT 1005
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O2-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
21.8%;
ery Match
21.8%;
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(HUMA-) HUMAN GENOME SCI INC.
ery Match
21.8%;
ery Match
80.5%;
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02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
21.8%;
ery Match 21.8%;
                                                                                                             Human immune/haematopoietic an WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                           (ISIS-) ISIS PHARM INC.
21.8%;
2ry Match
2t Local Similarity 76.9%;
                                                                                                                                                              (SAGR-) SAGRES DISCOVERY.
(SAGR-) SAGRES DISCOVERY.
21.8%;
ATY Match 21.8%;
The Local Similarity 78.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human reproductive system related WO200155320-A2.
                                Nucleotide sequence
WO200050593-A1
                                                      AAA64140 standard;
                                                                          (HUMA-) HUMAN GENOME SCI INC.

TY Match 21.8%;

t Local Similarity 79.6%;
                                                                                                                                                                                               Human genomic se
WO2003073826-A2.
12-SEP-2003.
                                                                                                                                                                                                                    ACN44490 standard; DNA; 32865 BP Human genomic sequence hCG25375.
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Human purinergic re
WO2003101177-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human P2X4 genomic US2004002152-A1.
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              (UYTE-)
                                                                                                                                                                                                                                                                                              Human genomic DNA
WO200155319-A2.
                                                                                                                                                                                                                                                                                                                    AAS32492 standard;
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(SEQU-) SEQUENOM INC.
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TENNESSEE RES CORP.
21.8%; Score 197.8;
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                                          DNA; 50000 BP.
e of a beta-tubulin
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21.8%;
77.9%;
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76.9%;
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4 gene
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No. 9.6
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No.
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No. 8.6e-46;
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No. 8.6e-46;
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. 1.1e-45;
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1e-45;
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9e-46;
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8.6e-46;
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9.1e-46;
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Best Local Similarity
RESULT 1009
ID AAD30228 stand*
DE Human PKD1
PN W020026
PD 24-"
PA
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Best Local Similarity
RESULT 1010
ID AAT94101 standard; D
BE Human PKD1 gene.
PN W09744457-A1.
PD 27-NOV-1997.
PA (GENZ) GENZYME CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
RESULT 1012
ID AAT94108 standard; DI
DE Human PKD1 locus beto
PN w09744457-A1.
PD 27-NOV-1997.
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DE
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Best Local Similarity
RESULT 1015
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RESULT 1017
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RESULT 1014
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                                                                                                                                                                             ACN44710 standard; DNA; 70242 BP.
Human genomic sequence hCG1784894.
W02003073826 A2.
12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
(SAGR-) SAGRES DISCOVERY.
Duery Match
21.8%; Score:
Best Local Similarity 80.7%; Pred. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-APR-1996.
(IGIG-) IG LAB INC.
(UYJO ) UNIV JOHNS HOPKINS.
21.8%; (UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                                                       AAK67283 standard; DNA; 68356 BP. Human immune/haematopoietic antig W0200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                        AAK83212 standard; DNA; 68356
Human immune/haematopoietic an
WO200157182-A2.
09-AUG-2001.
                                                                                                                                 Drug therapy altered expressed WO2004072265-A2.
                                                                                                                                                                                                                                                                                                                09-AUG-2001
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(GENZ ) GENZYME CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human polycystic WO9612033-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT18551 standard; DNA; 53577 BP. Human polycystic kidney disease n
ABK12169 standard; DNA; 98690 BP.
Human DNA representing the Tachykinin Receptor 1,
                                                                                                                       26-AUG-2004.
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                                                                                                (BURC/)
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                                                                                                           AMHP )
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                                                                                                           WYETH.
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                                    Similarity
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                                                                                  BURCZYNSKI M.
TWINE N.
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21.8%; Score
y 80.5%; Pred. 1
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21.8%;
80.5%;
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Te 197.8; 1
L. No. 1.2e
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No. 1.3
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No.
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No. 1.3e-45;
                                    197.8; DB 13;
No. 1.5e-45;
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No. 1.3e-45;
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No. 1.2e-45;
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No. 1.2e-45;
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                                              Length 96256;
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Query Match
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Best Local Similarity
RESULT 1018
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28-FEB-2002.
(GENA-) GENAISSANCE PHARM INC.
21.8%; Scr
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11-APR-2002.

(GENB-) GENE LOGIC INC.

21.8%;

21.8%;

21.8%;
                                                                                                                                                                                                                                                                                                                                                          ACA64895 standard; DNA; 134292
Human GABBR1 DNA corresponding
DE10127572-A1.
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(SAGR-) SAGRES DISCOVERY.
21-8%;
21-8%;
21-8%;
21-8%;
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Human IDE gene DNA sequence SeqID186.
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                                                                                                                                                                    AAZ86967 standard; DNA; 162450 BP. Retinoblastoma binding protein-7 cw020000607-A1.
                                                                                                                                                                                                                                                               ABK83562 standard; cDNA; 139904 BP Human cDNA differentially expressed WC200228999-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE43581 standard;
                                                                            ADE43315 standard; DNA; 2
Human IDE/ KNSL1 genomic
WO2003054143-A2.
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ry Match 21.8%;
t Local Similarity 80.7%;
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                                                                                                                                               GEST ) GENSET.
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                     ocal Similarity
                                                       NEUROGENETICS INC
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DNA;
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79.6%;
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79.6%;
                    CORP.
21.8%;
79.6%;
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No. 1.7e-45;
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No. 1.
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No. 1.7e-45;
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No. 1.7e-45;
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No. 1.6e-45;
                                                                                                                                                                                                                      197.8; DB 6;
No. 1.8e-45;
                       197.8; DB 10;
No. 2e-45;
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.5e-45;
                                                                                                                                                                                     DNA
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                                                                                                                                       Length 162450;
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                                   Length 202100;
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Best Local Similarity
RESULT 1028
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RESULT 1027
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(KETC/) KETCHUM K A.
(DFRA/) DI FRANCESCO V
(BEAS/) BEASLEY E M.
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(KETC/) KETCHUM K A.
(DFRA/) DI FRANCESCO V
(BEAS/) BEASLEY E M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS43104 standard; DNA; 325791 BP. Human Oestrogen receptor beta gene WO200162793-A2.
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04-DEC-2003.
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rry Match 21.8%; Score 197.
rt Local Similarity 82.3%; Pred. No.
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                                                                              EP1074617-A2.
                                                                                                                                                                     Human cancer suppressing CN1368508-A.
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(UNIV-) UNIVERSITAETSKLINIKUM FREIBURG
21.8%; Score 197
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Human protein tyrosine phosphatase 11
                                                                                                    AAH14398 standard;
                                                                                                                        (SHAN-) SHANGHAI INST ONCOLOGY.

ry Match 21.8%; Score
t Local Similarity 77.0%; Pred.
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                                                    (HELI-) HELIX RES INST.
                                                                                       Human cDNA sequence
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          ABK35751 standard;
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                                ocal Similarity
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 #142
cDNA; 2702 BP.
encoding novel human
                                                                                        cDNA; 2182 BP.
s SEQ ID NO:11832.
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21.8%;
79.6%;
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No. 2e-45;
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No. 4e
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No. 2.5e-46;
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2.5e-46;
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 secreted
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                                    46;
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O9-AL
(HUMA-)
Query Match
Best Local &
RESULT 1039
ID AAS28'
DB Gen'
PN W'
Query Match
Best Local S:
RESULT 1043
ID ADG41702 s
DE Human ress
PN US20032156
PD 20-NOV-200
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RESULT 1036
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Best Local Similarity
RESULT 1035
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Human immune/haematopoietic anti
W0200157182-A2.
09-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
Nery Match 21.8%; Sco
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O9-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
21.8%;
ery Match 21.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immune/haematopoietic antigen WO200157182-A2.
                                                                                             ADB33334 standard; DNA; 23626 BP.
Human novel lung related polypeptide
US2003054368-A1.
                                                                                                                                                                                                                                                                                                                                                        Genomic sequence #346 encoding WO200155448-A1.
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WO200277257-A1.
03-OCT-2002.
           Human respiratory system associated US2003215893-A1.
                               ADG41702 standard; DNA;
                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
ry Match 21.8%;
t Local Similarity 77.1%;
                                                                                                                                                                                 Human lung anti
                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
ry Match 21.8%;
t Local Similarity 77.1%;
                                                                                                                                                                                                                                                             Human nervous system WO200159063-A2. 16-AUG-2001.
                                                                                                                                                                                                                                                                                           ABA21480 standard;
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(HUMA-) HUMAN GENOME
                                                                         (HUMA-) HUMAN GENOME
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ry Match 21.8%;
t Local Similarity 77.1%;
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ity 84.3%;
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genomic DNA #67
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21.8%; ;
77.1%; ;
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No. 1e-45;
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No. 4.9e-46;
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No. 4.4e-46;
                    genomic
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1e-45;
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Query
Best Loc.
RESULT 1048
ID ADB333
DE Humar
PN US?
PD 2'
PA
PA
Best Local Similarity
RESULT 1052
ID ADA03092 standard; I
DE Human LFNG carcinoma
PN W02003057146-A2.
PD 17-JUL-2003.
                                                                                    Best Local Similarity
RESULT 1051
ID ADI:27170 standard; D
DE Human genomic sequen
PN US2003216558-A1.
PD 20-NOV-2003.
PA (MORR/) MORRIS D W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
RESULT 1047
ID AAS29998 standard; D
DE Human lung antigen g
PN w0200155303-A2.
PD 02-AUG-2001.
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RESULT 1046
ID ABA21481 standard; D
DE Human nervous system
PN W0200159063-A2.
PD 16-AUG-2001
PA (HUMA-) HUMAN GENOME
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Best Local Similarity
RESULT 1050
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RESULT 1044
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          Human LFNG carcinoma associated WO2003057146-A2.
                                                                                                                                                                                        24-APR-2003
                                                                                                                                                                                                Human respiratory system US2003077704-A1.
                                                                                                                                                                                                                        ADI97477 standard;
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02-AUG-2001.
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                               ADA03092 standard; DNA; 29322
                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                              ADG41703 standard;
                                                                                                                                                                                                                                                                                                                                                                                                     ADB33335 standard; DNA; 23632
                                                                            (ENGE/) ENGELHARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABA21481 standard; DNA; 23632 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME
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                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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ch 21.8%;
l Similarity 77.1%;
                                                                                                                                                                            HUMAN GENOME
                                                                                                                      sequence
                                                                                                                                                                                                                                                                                                               DNA; 23632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA; 23632 BP.
genomic DNA #68.
                                                                                                                                                                                                                        DNA;
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                                                                                                                                                      SCI INC.
21.8%;
77.1%;
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77.1%;
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21.8%;
77.1%;
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21.8%;
77.1%;
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84.3%;
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77.1%;
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77.1%;
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                                                                                                                      29040 BP.
for LFNG.
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                    gene,
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                                                      197
No.
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No. le-
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No.
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No.
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No. 1e-45;
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No. 1e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               novel human
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No. 1e-
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No. 1e-45;
                                                                                                                                                                                                            polypeptide-related
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                    SEQ
                                                     1.1e-45;
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. 1e-45;
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1е;
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-45;
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-45;
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                      ID NO:1610
                                                                                                                                                                                                                                                                                                    DNA
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(SAGR-)
(SAGR-)
Query Match
Best Local f
RESULT 1059
ID ABD33'
DE Hum'
PN WC
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Query Match
Best Local
RESULT 1
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RESULT 1055
ID AARGOGO
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                                                    Best Local Similarity RESULT 1061
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Human LENG 3-1.

MO2003008583-A2.

30-JAN-2003.

(SAGR-) SAGRES DISCOVERY.

(SAGR-) SAGRES DISCOVERY.

21.8%; 6
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09-AUG-2001.

(HUMA-) HUMAN GENOME SCI INC.

21.8%; /

21.8%; /

21.4%;
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Human LPNG gene genomic DNA sequence.
WO2003053224-A2.
03-JUL-2003.
                                                                                                                                                                                                                                                                                                    ACN44534 standard; DNA; 39768 BP. Human genomic sequence hCG38101. WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immune/haematopoietic wO200157182-A2.
                                                                                                                                                                                                         ABD33318 standard; DNA; 52987 BP. Human cancer-associated (CA) gene W02004058146-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME
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                                                                                                                           ACC45150 standard; DNA; 96649 Human NAC nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                 WO2004034995-A2.
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ry Match 21.8%;
t Local Similarity 84.3%;
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ry Match 21.8%;
t Local Similarity 80.3%;
                                                                                                                WO2003024988-A1.
                                                                                                                                                             (SAGR-) SAGRES DISCOVERY INC.
ry Match 21.8%;
t Local Similarity 77.1%;
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                     Local Similarity
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Similarity
                                                                  S PHARM INC.
21.8%;
ilarity 80.3%;
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74.4%;
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78.1%;
21.8%;
73.6%;
                                 21.8%;
73.6%;
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Pred.
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Pred.
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Pred.
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Pred.
Score
Pred.
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Pred.
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Pred.
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                                                                   197.6;
No. 1.7
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No. 1.2e-45;
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No. 1.1e-45;
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No. 1.1e-45;
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No. 1.1e-45;
 197.6; DB 12;
No. 1.8e-45;
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No. 1.2e-45;
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No. 1.2e-45;
                                 197.6; DB 10;
No. 1.8e-45;
                                                                                                                                                                197.6; DB 13;
No. 1.4e-45;
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                                                                                                                              NO:10
                                                                     1.7e-45;
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Query Match
Best Local Similarity
RESULT 1066
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RESULT 1070
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                                    Query Match
Best Local Similarity
RESULT 1072
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05-DEC 2002.

05-DEC 2002.

(PATH-) PATHOARRAY GMBH.

(PATH-) PATHOARRAY GMBH.

21.8%;

ery Match 21.11arity 84.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INCY-) INCYTE GENOMICS INC.
ery Match 21.8%;
st Local Similarity 76.6%;
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PRY Match 21.8%; Sco
t Local Similarity 76.6%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENB-) GENE LOGIC INC.
21.8%;
rry Match 21.8%;
rt Local Similarity 76.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA differentially expressed WO200228999-A2.
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                                                                          Human kinase genomic
                                                                                                                                                                                                                                                       ADN16204 standard; DNA; 260209
Human sulfatase SULF1 gene.
WO2004031365-A2.
                                                                                                                                                                                                                                                                                                                                                                              ABS56564 standard; DNA; 260209 BP.
Human SULF2 genomic DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACN44010 standard; DNA; 198522 BP. Human genomic sequence hCG1643869. WO2003773826-A2.
           ACH36634 standard;
Human endothelial
                                                                                                                                                              ABK89296 standard; DNA; 326014 BP
                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA. (THIO-) THIOS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                   WO200259327-Ā2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK83571 standard; cDNA; 175737 BP.
                                                                                          ADQ94981 standard; DNA; 326014 BP.
                                                                                                                                                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA.
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US2003073623-A1.
                                                                                                                     gene for novel serine/threonine
tch 21.8%; Score 197
al Similarity 80.3%; Pred. No.
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              cell cDNA
                                                                                                                                                                                       21.8%;
86.9%;
                                                                                                                                                                                                                                                                                                                21.8%;
86.9%;
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78.7%;
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               #4767
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U07000.
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No. 2.6
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No. 2.2e-45;
                                                     197.6; DB 12;
No. 2.8e-45;
                                                                                                                      197.6; DB 6;
No. 2.8e-45;
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No.
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No.
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No. 2.1e-45;
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No. 2.6e-45;
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                                                                                                                                              serine kinase
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2.2e-45;
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2.2e-45;
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2.3e-45;
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.6e-45;
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                                                                  Length 326014;
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                                                                                                                                       326014;
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Best Local Similarity
RESULT 1079
ID ABD33470 standard; I
DE Human cancer-associa
PN w02004058146-A2.
PD 15-JUL-2004.
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RESULT 1073
ID ADB83200 standard; c
DE Human cDNA sequence
PN W02003050236-A2.
PD 19-JUN-2003.
PA (CHIR) CHIRON CORP.
                                                                                         Best Local Similarity RESULT 1080
                                                                                                                                                                                                                                                   Best Local Similarity RESULT 1078
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Best Local Similarity
RESULT 1076
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RESULT 1074
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                                                                                                                                                                                                                                                       Human digestive system antige WO20015314-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADG10849 standard; cDNA; 1599 BP.
Human STAT6-activating protein-encoding
W0200296943-A1.
05-DEC-2002.
(ASAH) ASAHI KASBI KOGYO KK.
                                                                                                                                        Human cancer-associated WO2004058146-A2.
                                                                                                                                                                                                                                                                                                                                                                        Human immune/haematopoietic anti
WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH98452 standard;
Human EST-derived of
WO200154477-A2.
                                                ACN44362 standard; DNA; 68255 BP.
Human genomic sequence hCG39597.
WO2003073826-A2.
                                                                                                                                                                                                                                ABD33436 standard; DNA; 52710 BP.
Human cancer-associated (CA) gene HD07-082.
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ry Match 21.8%;
t Local Similarity 82.1%;
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(HYSE-) HYSEQ INC.
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                  (SAGR-) SAGRES DISCOVERY.

ry Match 21.8%;
Local Similarity 73.3%;
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) DICKSON M C.
) JONES L W.
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No. 6.4e-46;
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No. 4.1e-46;
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No.
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No. 2.5e-46;
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5.8e-46;
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1.7e-45;
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                               68255;
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20-MAR-2003.
(ISIS-) ISIS PHARM INC.
(ISIS-) 21.7%;
21.7%;
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                                                          Human cDNA sequence
                                                                       AAH16580 standard;
                                                                                                                               ACC86725 standard; DNA; 751 BP.
Human VEGFR-1 nucleotide sequence
WO2003022227-A2.
20-MAR-2003.
                                                                                                                                                                                                                                                     ABN61073 standard; cDNA; 662 Human cancer related polynucl WO200214500-A2.
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US5597694-A.
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Consensus Alu repeat sequence.
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(HELI-) HELIX RES INST.
ry Match 21.
t Local Similarity 82.
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(HYSE-) HYSEQ INC.
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ry Match 21.7%; Sc
t Local Similarity 72.4%; Pr
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ry Match 21.8%;
t Local Similarity 83.7%;
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tch 21.7%; Score 197
al Similarity 81.9%; Pred. No.
                                                          cDNA;
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No. 5.2e-46;
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No. 2.1e-45;
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No. 2.1e-45;
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No. 2.1e-45;
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RESULT 1095
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WO2003039443-A2.
                                                  AAK89986 standard; DNA; 32224 BP.
Human digestive system antigen ge
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WO200157182-A2.
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(HUMA-) HUMAN GENOME
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(HUMA-) HUMAN GENOME
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(HUMA-) HUMAN GENOME
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                                          WO200155314-A2.
                                                                                   (HUMA-) HUMAN GENOME SCI INC.
ry Match 21.7%;
t Local Similarity 81.8%;
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(SCHO/) SCHOCH C.
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Query Match
Best Local Similarity
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Best Local Similarity
RESULT 1104
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Best Local Similarity
RESULT 1103
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05-FEB-2004.
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17-JUL-2003.
(SAGR-) SAGRES DISCOVERY.
21-7%;
21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%; 21-7%;
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Gene #3328 used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABD33190 standard; DNA;
Human cancer-associated
WO2004058146-A2.
15-JUL-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human MYB gene. w02003008583-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human MYB carcinoma associated WO2003057146-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune/haematopoietic WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ISIS-) ISIS PHARM INC.
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(SAGR-) SAGRES DISCOVERY.

ry Match 21.7%;

t Local Similarity 80.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human MYB gene g
WO2003039484-A2.
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Human MYB gene genomic DNA
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ry Match 21.7%;
t Local Similarity 84.2%;
                                                                                                                                                                                                                                                                                                                          92Kb gene fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB72266 standard;
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                                                                                                                                                AAD53224 standard;
                                                                                                                                                                                                                                                                                                   WO200210455-A2.
                                                                                                                                                                                                                                                                                                                                            AAD31364 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME
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                                                                                                                            Human chromosome
                                                                                                                                                                                                                                      (CELL-) CELLTECH R
(STRA/) STRAEHLING
                                        (DELA/) DELATYCKI
                                                                                                                                                                                           Local Similarity
                                                                 MURDOCH CHILDRENS RES
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diagnose liver
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                                                                                                                            DNA; 567571 BP.
q-arm breakpoint
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80.3%;
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85.8%;
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DNA #3.
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(CA) gene
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Pred.
Score 197.2; DB 8; Pred. No. 2.4e-45;
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No. 1.6
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No. 1.5
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No. 2e-
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No.
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No. 1.9e-45;
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No. 1.9e-45;
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No. 2.1e-45;
                                                                                                                              region
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.2e-45;
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-45;
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Best Local Similarity
RESULT 1120
ID ARTESTS
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RESULT 1116
                                                      Best Local Similarity RESULT 1121
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                                                                                                      Human protein synthesis initiation CN1331221-A.
                                                                                                                                                                                                 Human genomic DI
WO200155319-A2.
                                                                                                                                                                                                                                                                                                  AAI95194 standard; o
Human neuroblastoma
WO200166719-A1.
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                    WO2003004989-A2.
                                 Breast
                                          ACC50229 standard;
                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
ry Match 21.7%;
t Local Similarity 82.4%;
                                                                                                                                                                                         02-AUG-2001
                                                                                                                                                                                                                       AAS32730 standard;
                                                                                                                                                                                                                                            (CHIB-) CHIBA PREFECTURE.
(HISM ) HISAMITSU PHAN, CO LTD.
ry Match 21.7%; Score
t Local Similarity 75.1%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                        Human cancer assu
WO2004060304-A2.
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13-OCT-2003.
(CELL-) CELLTECH R & D INC.
(CELL-) CELLTECH R & D INC.
(UYRO-) UNIV ROTTERDAM ERASMUS.
(UYRO-) UNIV ROTTERDAM ERASMUS.
R0.5%; Pred.
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WO2004063709-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADQ80254 standard;
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ry Match 21.7%; Score
t Local Similarity 78.6%; Pred.
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                                                                                     (BODE-) BODE GENE DEV CO LTD
                                                                                                                                                                                                                                                                                                                                            (SAGR-) SAGRES DISCOVERY INC.
ry Match 21.7%;
Local Similarity 84.5%;
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associated
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PHARM INC
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yndrome associated
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                                                                21.7%;
80.0%;
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74.0%;
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                                                               SHANGHAI.
Score 197; DB 6;
Pred. No. 6.3e-46;
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d polynucleotide
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No.
                                                                                                                      factor 10.12-encoding
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No. 2.4e-45;
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No. 2.4e-45;
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No. 2.4e-45;
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                                                                                                                                                                                                           antigen,
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2.5e-45;
                               SEQ
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2.5e-45;
                                                                                                                                                       .2e-
                                                                                                                                                                                                                                                                                                                                                                                                                                      ; DB 10;
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.6e~45;
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                                 NO:301
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Best Local Similarity
RESULT 1129
ID ABD32570 standard; D
DE Human cancer-associa
PN w02004074320-A2.
PD 02-SEP-2004.
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Best Local Similarity
RESULT 1122
ID ADRO7810 standard; c
DE Full length human cD
PN EP1447413-A.
PD 18-AUG-2004.
                                                                                                                                                                                                                                         Query Match
Best Local Similarity
RESULT 1128
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Best Local Similarity
RESULT 1126
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RESULT 1125
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RESULT 1124
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                   Human cancer-assum02004058146-A2.
                                                                                                             Human cancer-associated WO2004074320-A2.
                                                                                                                                                               Human digestive system antigen w0200155314-A2.
02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ery Match
21.7%; Sc
st Local Similarity 82.5%; Pr
                                                                                                                                                                                                                                                                                              Human digestive WO200155314-A2.
                                                                                                                                                                                                                                                                                                         AAK89550 standard; DNA; 13246 E
Human digestive system antigen
                                                                                                                                                                                                                                                                                                                                                                                              AAZ59353 standard;
Human STP2 (phenol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAK85025 standard; DNA; 5919 BP
Human immune/haematopoietic antigen
                                                     ABD33137 standard;
                                                                                                                                                                                                                               AAK89551 standard; DNA; 13247 BP.
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                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
ry Match 21.7%;
t Local Similarity 82.5%;
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EP1447413-A2.
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RY Match 21.7%; Scot Local Similarity 78.9%; Pre
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ry Match 21.7%; Score
t Local Similarity 83.7%; Pred.
                                                                                                (SAGR-) SAGRES DISCOVERY INC.
                                                                                                                                                                                                                                                                                                                                       (AXYS-) AXYS PHARM INC.
ry Match 21.7%;
Local Similarity 74.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
ry Match 21.7%;
t Local Similarity 79.2%;
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                                                                           Local Similarity
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human cDNA useful
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human cDNA useful
                                          ndard; DNA;
-associated
DISCOVERY INC.
21.7%;
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77.9%;
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78.9%;
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genomic DI
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(CA) g
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                                        6 BP.
gene
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197;
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No. 1
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No. 1.
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No. 1.
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No. 1e-45;
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No. 8.
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No. 7.
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No. 7.
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No. 6.
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No. 7.5e-46;
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.5e-45;
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.8e-46;
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 BB
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.5е-
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 Length 22056;
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Best Local Similarity
RESULT 1131
ID AAFOIT
Best Local Similarity
RESULT 1139
ID ACN44082 standard; E
DE Human genomic sequen
PN W02003073826-A2.
PD 12-SEP-2003.
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Best I
RESULT 1
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Best Local Similarity
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(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

21.7%; Score 197; DB 10;

ery Match
21.7%; Pred. No. 1.6e-45;
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02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
21.7%;
217 Match 21.7%;
21.7%;
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02-AUG-2001.
(HUMA-) HUMAN GENOMB SCI INC.
21.7%;
21.7%;
21.7%;
21.7%;
21.7%;
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Human colorectal cancer antigen coding sequence
WO200155350-A1.
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Human digestive system antigen genomic sequence
WO200155314-A2.
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Human GPCR gene SEQ ID NO:2037.
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                                                                                                                                                                                                                        ADQ59482 standard; DNA; Human cancer-associated WO2004058288-A1.
                                                                                                                                                                                                                                                                                                                             ADB93003 standard; DNA; 32199
Human colorectal cancer relate
US2003054420-Al.
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                                                                                                                   ACN45130 standard; DNA; 61197 BP
Human genomic sequence hCG15017.
WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABS99850 standard;
              Human genomic sequence hCG39199.
WO2003073826-A2.
                                        ACN44082 standard; DNA; 71048 BP
                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                         (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                               (SAGR-) SAGRES DISCOVERY.
ry Match 21.7%;
Local Similarity 77.3%;
                                                                                                                                                                                             (SAGR-) SAGRES DISCOVERY INC.
                                                                                                                                                           Local Similarity
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                                                                                                                                                                       21.7%;
79.5%;
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74.2%;
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ig human colorectal cancer related
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(CA) 9
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related polypeptide DNA
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No. 1.
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No. 1.
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No. 1
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No. 1.7e-45;
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No. 2.
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No. 1.7e-45;
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.7e-45;
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.7e-45;
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.6e-45;
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.9e-45;
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.2e-45;
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Best Local Similarity
RESULT 1149
ID ADH54060 standard; D
DE Human IDE gene varia
PN US2003224380-A1.
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Best Local Similarity
RESULT 1140
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Best Local Similarity
RESULT 1145
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Best Local Similarity
RESULT 1142
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RESULT 1147
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RESULT 1148
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Polymorphic human II
WO2003054143-A2.
03-JUL-2003.
                                               04-DEC-2003.
04-DEC-2003.
(GEMO ) GEN HOSPITAL CORP.
(GEMO ) 21.7%;
ery Match 21.7%;
ery Match 80.0%;
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EXY Match 21.7%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Human G-protein coupled
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                                                                                                                                                                                                        ADE43581 standard; DNA; 128034 BP
Human IDE genomic sequence, SEQ II
WO2003054143-A2.
03-JUL-2003.
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Human genomic sequence hCG18576.
WO2003073826-A2.
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(INSP ) INST PASTEUR.
                                                                                                      Human IDE gene DNA
US2003224380-A1.
                                                                                                                               ADH54059 standard;
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(SAGR-) SAGRES DISCOVERY.

ry Match 21.7%;

t Local Similarity 79.2%;
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ry Match 21.7%;
t Local Similarity 80.0%;
             ADH54060 standard; DNA; 128
Human IDE gene variant DNA
                                                                                                                                                        (GEHO ) GEN HOSPITAL CORP.
ry Match 21.7%;
t Local Similarity 80.0%;
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cy Match 21.7%;
Local Similarity 79.8%;
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c DNA.
                                                                                                                  DNA; 128034 BP.
sequence SeqID186.
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80.0%;
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21.7%; Score 197;
77.3%; Pred. No.
                             128034 BP.
             sequence SeqID187
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No. 2.7e-45;
                                                     197; DB 12;
No. 2.9e-45;
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No. 2.8e-45;
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No. 2.3e-45;
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.8e-45;
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.8e-45;
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.8e-45;
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.9e-45;
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03-JUL-2003.
(INCY-) INCYTE GENOMICS INC.
21.7%;
erv Match 21.7%;
84.0%;
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WO2003073826-A2.
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12-SEP-2003.

(SAGR-) SAGRES DISCOVERY.

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10-JUN-2004.
(PROT-) PROTEIN DESIGN LABS
21.7%;
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12-SEP-2003.
(SAGR-) SAGRES DISCOVERY.
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ADQ86839 standard; cDNA; Human tumour-associated & WO2004060270-A2.
                                                                                                Human cDNA en
EP1308459-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACN43946 standard; DNA; 174448 BP Human genomic sequence hCG21793. WO2003073826-A2.
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Human soft tissue &
WO2004048938-A2.
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Human soft tissue sarcoma-upregulated
                                                                                                                                                                                                                                  (SAGR-) SAGRES DISCOVERY.
ry Match 21.7%;
t Local Similarity 77.1%;
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ry Match 21.7%; Score
t Local Similarity 82.5%; Pred.
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                                                                (HELI-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                       ADB62528 standard;
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                                                                                                            cDNA encoding
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g clone HHDPC20082790
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on containing the
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No. 3.
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No. 2.9e-45;
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7e-46;
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1.9e-45;
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1.1e-45;
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.5e-45;
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.2e-45;
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Best Local Similarity
RESULT 1166
ID ADQ24919 standard; D
DE Human soft tissue sa
PN W02004048938-A2.
PD 10-JUN-2004.
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RESULT 1162
ID ACN40563 standard; c
DE Tumour-associated an
PN W02004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH IN
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Best Local Similarity
RESULT 1161
ID ADQ84044 standard; c
DE Human tumour-associa
PN W02004060270-A2.
PD 22-JUL-2004.
PA (GETH.) GENENTECH IN
                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 1163
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(GETH ) GENENTECH I
(WUTD/) WU T D.
(ZHOU/) ZHOU Y.
          ADQ24919 standard; DNA; 6833 BP. Human soft tissue sarcoma-upregulated WO2004048938-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human tumour-associated a WO2004060270-A2.
                                                                                                        AAK66744 standard; DNA; 5079
Human immune/haematopoietic a
                                                                                                                                                                       CN1345948-A.
24-APR-2002.
                                                                                                                                                                                             ABQ83600 standard; cDNA; 2631 BP.
Human fumarate reductase/succinic dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADQ84044 standard; cDNA;
Human tumour-associated a
WO2004060270-A2.
22-JUL-2004.
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                                                                                                                                                                                                                                                                                                                (GETH) GENENTECH INC.
ry Match 21.7%;
t Local Similarity 80.5%;
                                                                                                                                        (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
ry Match
21.7%; Score 196.8; DB 6;
t Local Similarity 84.7%; Pred. No. 7.4e-46;
                                                                                                                                                                                                                                                                                                                                                                                 ACN40563 standard; cDNA; 2320
                                                                                                                                                                                                                                                   (REAS-) RES ASSOC BIOTECHNOLOGY
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) WU T D.
) ZHOU Y.
                                                                          HUMAN GENOME
                                                                                                                                                                                                                                                                                  ; cDNA; 2404 BP. invention SEQ ID
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No. 7e-
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No. 7e-46;
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No.
                                                                                                          genomic
                      DNA -
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7.1e-46;
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Best Local
Best Local
RESULT 1168
ID AAIC
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RESULT 1169
ID AAL06760
RESULT
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09-AUG-2001.

(HUMA-) HUMAN GENOME SCI INC.

(HUMA-) HUMAN GENOME SCI INC.

21.7%;

ery Match 21.7%;
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Human soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                ABL98683 standard; DNA; 7444 BP.
Human testicular antigen encoding DNA fragment SEQ
W0200155317-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human reproductive system WO200155320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAL06118 standard;
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ry Match 21.7%; Sco

t Local Similarity 84.7%; Pre
                                                                                                                  Human immunoglobulin encoding WO200155315-A2.
                                                                                                                                                                                                                                                                                                     Human nervous system related WO200159063-A2.
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(HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                       AAK66749 standard; DNA; 9324 BP.
Human immune/haematopoietic antigen genomic sequence
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(HUMA-) HUMAN GENOME
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                                                                                                                                           AAS28895 standard; DNA; 9765 BP.
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                                    AAS28886 standard; DNA; 9765 BP.
Human immunoglobulin encoding genomic
                                                                                                                                                                                                              40200157182-A2.
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ry Match 21.7%;
Local Similarity 83.4%;
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                                                                      (HUMA-) HUMAN GENOME SCI INC.
CY Match 21.7%;
Local Similarity 78.0%;
                                                           Local Similarity
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21.7%;
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21.7%;
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polynucleotide
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No.
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No. 1.1e-45;
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No. 1.1e-45;
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No. 1.1e-45;
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No.
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No. 1.2e-45;
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1.1e-45;
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HUMAN GENOME

SCI

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RESULT 1176
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RESULT 1184
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RESULT 1181
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Human genomic DNA SEQ ID NO:
WC200154474-A2.
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:ry Match 21.7%;

:t Local Similarity 78.0%;
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Human novel protein DNA
US2003077606-A1.
                                                                                                                                                                                                                                                                                                                              Human novel protein US2003077606-A1.
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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Human polynucleotide SEQ
US2002090672-A1.
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C
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                                                                              ABA15617 standard; DNA; 15186 BP.
Human nervous system related poly
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Human nervous system related
                                                                       WO200159063-A2.
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         BA15616 standard; DNA; 15187 BP.
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                             HUMAN GENOME SCI INC. h 21.7%; Similarity 82.0%;
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21.7%; S
larity 80.5%; F
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de SEQ ID NO (
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No. 1.4e-45;
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No. 1.2e-45;
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No. 1.2e-45;
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No. 1.2e-45;
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1.2e-45;
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RESULT 1190
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RESULT
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Genomic DNA encoding I
WO200264626-A2.
22-AUG-2002.
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09-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) 21.7%;
ery Match 21.7%;
83.2%;
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09-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) 21.7%;
ery Match 21.7%;
83.2%;
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02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
21.7%;
ery Match 21.7%;
79.5%;
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22-JUL-2004,
22-JUL-2004,
(SAGR-) SAGRES DISCOVERY INC.
(SAGR-) SAGRES DISCOVERY INC.
21.7%;
ery Match 21.7%;
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(02-JAN-2003.

(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY (NASC-) CENT ADVANCED SCI & TECHNOLOGY INCUBAT: (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBAT: ery Match 21.7%; Score 196.8; DB ery Match 29.5%; Pred. No. 1.7e-45
                                                                                                                                                                                                                                                                                                  Human cancer associated sequence HD08-012, WC2004060304-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADQ97776 standard; DNA; 25694 BP. Human cancer associated sequence HD10-045, WO2004060304-A2.
ABX60280 standard; cDNA; 32192 BP.
cDNA encoding novel human musculoskeletal system antigen #2624.
                                                                                                                                                                                                             AAL37292 standard; DNA; 32192 BP.
Human musculoskeletal system related polynucleotide
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Human GPCR gene SEQ ID NO:621.
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Human immune/haematopoietic antigen genomic sequence
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                                      (HUMA-) HUMAN GENOME SCI INC.
ry Match 21.7%;
t Local Similarity 79.5%;
                                                                                         Human reproductive WO200155320-A2.
                                                                                                                     AAL07103 standard;
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ry Match 21.7%;
t Local Similarity 82.0%;
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Pred. No. 1.8e-45;
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Score 196.8; DB 10;
Pred. No. 1.7e-45;
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No. 1.5e-45;
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No. 1.5e-45;
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1.9e-45;
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1.8e-45;
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(CAND/) GARMAN J L
(CAND/) CANDIA A F.
Query Match
Best Local Similarity
RESULT 1200
ID ADA02960 stand
DB Human DATT
PN WO277
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RESULT 1194
ID ADDITION
                                                                                                                                                                                                                                    Best Local Similarity
RESULT 1198
ID ADJ12847 standard; DN
DE DNA fragment of a BAC
PN US2004010132-A1.
PA (ROSE) ROSEN C A.
PA (ROSE) BREWER L A.
PA (BREW) BREWER L A.
PA (DUAN) DUAN R D.
PA (FLOR) FLORENCE K A.
PA (GREE) GREENE J M.
PA (FUR) FLORENE S M.
PA (FUR) FLORENE S M.
PA (FUR) FLORENE C C.
PA (TUG) TO GREENE C C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
RESULT 1196
ID ABN95727 standard; Dr
DE Gene #2225 used to di
PN W0200229103-A2.
PD 11-APR-2002.
                                                                                                            Query Match
Best Local Similarity
RESULT 1199
ID ABK85018 standard; D
Human cadherin-like
PN W0200231117-A2.
PD 18-ABR-2002.
PA (ARBO-) ARBOR VITA C
PA (GARM/) GARMAN J D.
PA (GARM/) GARMAN J D.
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Best Local S
RESULT 1195
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                 ADA02960 standard; DNA; 44325 BP. Human DAD1 carcinoma associated g WO2003057146-A2.
                                                                                                                                        Human cadherin-like WO200231117-A2. 18-APR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune/haematopoietic WO200157182-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                    DNA fragment of a BAC US2004010132-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADJ12847 standard; DNA; 37925 BP DNA fragment of a BAC clone that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAK72372 standard;
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10-OCT-2002.
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ry Match 21.7%;
t Local Similarity 79.5%;
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GREENE J M.
YOUNG P E.
FERRIE A M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           യ വ
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82.0%;
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topoietic antigen genomic sequence
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diagnose liver
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76.9%;
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79.5%;
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Pred.
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Pred. No. 1.9
                                                                                                                                                                   BP.
protein-2
                               gene,
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No. 2e-
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No. 2.1e-45;
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No. 2.1e-45;
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No.
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No. 1.9e-45;
                                SEQ ID NO:1478
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1.9e-45;
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                                                                       ; DB 6;
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-45;
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                                                                                      43545;
                                                                                                                                                                        DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                 protein Seq701.
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Best Loca.
RESULT 1202
ID ADC°
DB
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Best Local S
RESULT 1204
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Best Local Similarity
RESULT 1201
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RESULT 1206
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                                                    P P P B G
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Best Local Similarity
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Human phospholipase A2 (PLA2), group VI (Ca2+-independent)
US6410325-B1.
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10-JAN-2003.

(SAGR-) SAGRES DISCOVERY.

(SAGR-) SAGRES DISCOVERY.

21.7%;

21.7%;

82.0%;
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Human DAD1 gene.
WO2003008583-A2.
                                                                                                                                                                                                                                                                                          ABD33432 standard; DNA; 106938 BP. Human cancer-associated (CA) gene HD07-081. W02004058146-A2.
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Human cancer-associated genomic DNA HD7-204.
WO2004074320-A2.
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                                                                            ADL17884 standard; cDNA; 158001 BP. Human phosphotyrosyl phosphatase ac US2004023906-A1.
                                                                                                                                                                                   Human cancer associated WO2004074321-A2.
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(SAGR-) SAGRES DISCOVERY INC.
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(SAGR-) 21.7%;
ry Match 21.7%;
L Local Similarity 82.0%;
 ACA64924 standard;
                                                                                                                        USAGR-) SAGRES DISCOVERY INC.
(SAGR-) SAGRES DISCOVERY INC.
21.7%;
ry Match 21.7%;
81.8%;
                                                                                                                                                                                                                                        (SAGR-) SAGRES DISCOVERY INC.
cy Match 21.7%;
Local Similarity 81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                (ISIS-) ISIS PHARM INC.
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(ENGE/) ENGELHARD E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                    Local Similarity
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h 21.7%;
Similarity 82.0%;
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21.7%;
84.5%;
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DNA; 201239 BP
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79.1%;
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Pred.
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                                                                                                                                 Score 196.8; DB 13; Pred. No. 3.1e-45;
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                                                                                                                                                                                                 genomic
                          Score 196.8; DB 1: Pred. No. 3.6e-45;
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                                                                                           activator, PTPA,
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No. 2.8e-45;
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No. 2.6e-45;
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No. 2.2e-45;
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No. 2.2e-45;
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2.2e-45;
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                                      DB 12;
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                                        Length 158001;
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Query Match
Best Local Similarity
RESULT 1213
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Query Match
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W020026317-A2.
24-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ovarian carcinoma WO200206317-A2. 24-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ovarian carcinoma antigen WO200036107-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PATH-) PATHOARRAY GMBH.
ry Match 21.7%;
t Local Similarity 80.7%;
                                                                                                                                                                                                                                                                                                                                                         Human ovarian carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABN72587 standard; DNA; 461 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA69693 standard; cDNA; 461
                                                                                                                                  US2003091580-A1.
15-MAY-2003.
                                                                                                                                                     Human ovarian carcinoma antigen polynucleotide
                                                                                                                                                                 ADA08750 standard; DNA; 461 BP.
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                                                                                                                                                                                                                                                                                                                                                                      ADA08752 standard; DNA;
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                                                                                                                                                                                                                                                                                                              (KING/)
                                                                                                                                                                                                           ) CARTER D.
) HILL P.
) ALBONE E.
                                                                                                                                                                                                                                                                                                 MITCHAM J L.
KING G E.
ALGATE P A.
          HILL P.
ALBONE E.
                                         KING G E.
ALGATE P A.
FLING S P.
RETTER M W.
FANGER G R.
REED S G.
VEDVICK T S.
                                                                                                                                                                                                                                           PLING S P.
RETTER M W.
FANGER G R.
REED S G.
VEDVICK T S.
                                                                                                                                                                                                                                                                                                                                                                                                                CORIXA CORP.
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72.4%;
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72.4%;
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Pred.
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                                                                                                                                                                                       Score
Pred.
 Score 196.6;
                                                                                                                                                                                                                                                                                                                                                          polynucleotide
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No. 3.9e-45;
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No. 4.3e-46;
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No. 4.3e-46;
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No. 4.3e-46;
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No. 4.3e-46;
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  DB
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  Length 461;
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Best Local Similarity
RESULT 1225
ID ACD41819 standard; c
DE Human secreted/trans
PN US2003036179-A1.
PD 20-FBB-2003.
PA (GETH) GENENTECH IN
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RESULT 1221
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RESULT 1218
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Best Local S
RESULT 1222
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Best Local Si
RESULT 1220
ID ADG46245 E
DE Human ovar
PN US20031655
PD 04-SEP-200
PA (RETT/) RE
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Best Local Similarity
RESULT 1224
                                                                                                                                                                                                                                                                  Best Local Similarity RESULT 1223 ID ACA03627 standard;
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SULT 1217
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                                                                                                                                ABX89165 standard;
DNA encoding novel
US2003017563-A1.
                                                                                                                                                                                                                                        CDNA encoding human US2003036180-A1.
                                                                                                                                                                                                                                                    ACA03627 standard; cDNA; 3719 BP. cDNA encoding human PRO polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP08499 standard; cDNA; 461 BP.
cDNA encoding secreted ovarian carcinoma
US2003124140-A1.
03-JUL-2003.
(CORI-) CORIXA CORP.
                          ACD41819 standard; cDNA; 371: Human secreted/transmembrane US2003036179-A1.
                                                                                                                                                                                  (GETH) GENENTECH INC.

(GETH) 21.7%;

TY MATCH 21.7%;

TOCAL Similarity 80.2%;
                                                                                                                                                                                                                                                                                                                                   Human cDNA sequence WO200140466-A2. 07-JUN-2001.
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(HELI-) 21.7%;
(TY Match 21.7%;
(Ty Local Similarity 80.2%;
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                                                                                                                                                                                                                                20-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                          07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cDNA sequence
EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH15355 standard; cDNA; 1652 BP.
Human cDNA sequence SEQ ID NO:13531
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04-SEP-2003.
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(CORI-) CORIXA CORP.
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(FANG/) FANGER G R.
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Pred.
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Pred. No. 9.6e-46;
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No. 9.6e-46;
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No. 7.1e-46;
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No. 4.3e-46;
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No. 4.3e-46;
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9.6e-46;
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Best Local Similarity
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PN US20
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Best Local Similarity
RESULT 1226
ID ACA04048 standard; c
DE Human cDNA encoding
PN US2003032155-A1.
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Best Local Similarity
RESULT 1232
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Best Local Similarity
RESULT 1230
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RESULT 1227
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20-MAR-2003.
(GETH) GENENTECH INC.
21.7%; (
Match 21-74 80.2%;
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01-MAY-2003.
(GETH ) GENENTECH INC.
21.7%;
Watch 21.7%;
                           Human PRO polynucleotide US2003087350-A1.
                                                                                                                Novel human secreted and US2003082711-A1.
                                                                             (GETH) GENENTECH INC. 21.7%;
PYY Match 21.7%;
St Local Similarity 80.2%;
                                                                                                                                                                                                cDNA encoding human PRO polypeptide US2003082704-A1.
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Human PRO polynucleotide #25.
US2003054517-A1.
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13-MAR-2003.
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A INC.
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ty 80.2%;
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RESULT 1236
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10-APR 2003.

(GETH ) GENENTECH INC.

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Human PRO polynucleotide #25.
US2003082763-A1.
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Human PRO polynucleotide #25.
US2003082705-A1.
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Human PRO polynucleotide
US2003068795-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2003073215-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA encoding human US2003068794-A1.
                                                   ADA91474 standard; cDNA; 3719 BP. Novel human secreted and transmem
                                                                                                                                   ADB16382 standard; cDNA;
Human PRO polynucleotide
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(GETH ) GENENTECH INC.
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RESULT 1244
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(GETH ) GENENTECH INC.

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Novel human secreted and transmembrane
US2003073211-A1.
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24-APR-2003.
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Human PRO polynucleotide #25.
                                     ADA81932 standard; cDNA;
Human PRO polynucleotide
US2003082701-A1.
01-MAY-2003.
                                                                                                                          ADB24408 standard; cDNA; 3719 BP.
Human PRO polynucleotide SEQ ID N
US2003077713-A1.
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Human PRO polynucleotide #25.
US2003073210-A1.
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                                                          ADA93144 standard; cDNA;
Human PRO polynucleotide
US2003077721-A1.
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Human PRO polynucleotide
US2003082761-A1.
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22-MAY-2003.
(GETH ) GENENTECH INC.
21.7%; 5
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                                                                             ADB21427 standard; cDNA; Novel human secreted and US2003082765-A1.
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Human PRO polynucleotide #25.
US2003082759-A1.
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24-APR-2003.
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US2003049817-A1.
13-MAR-2003.
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ADA77206 standard; cDNA; 3719
Human PRO polynucleotide #25.
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No. 9.6e-46;
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No. 9.6e-46;
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No. 9.6e-46;
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US2003068797-A1.

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RESULT 1272

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ID ADA97289 standard; co
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24-APR-2003.
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Novel human secreted and transmembrane
  ADA97289 standard; cDNA;
Human PRO polynucleotide
US2003082686-A1.
                                                                                             Novel human secreted and US2003073213-A1.
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Human PRO polynucleotide #25.
US2003059909-A1.
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        Novel human secreted and transmem. US2003087347-A1.
08-MAY-2003.
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US2003068793-A1.
                                                                                                      ADB38341 standard; cDNA; 3719 BP.
Novel human secreted and transmembrane
US2003082766-A1.
01-MAY-2003.
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Human PRO polynucleotide
US2003087352-A1.
08-MAY-2003.
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Human PRO polynucleotide SEQ ID 1
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ry Match 21.7%;
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Novel human secreted and
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01-MAY-2003.
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24-APR-2003.
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Best Local Similarity
RESULT 1290
ID ADB66261 standard; c
DE Novel human secreted
PN US2003082689-A1.
PD 01-MAY-2003.
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RESULT 1296
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RESULT 1294
ID ADB46797 standard;
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RESULT 1291
ID ADB89341 standard;
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(GETH ) GENENTECH INC.
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(GETH) GENENTECH INC.

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Novel human secreted and
US2003082689-A1.
01-MAY-2003.
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Human PRO polynucleotide
US2003082762-A1.
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(GETH ) GENENTECH INC.

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Human PRO polynucleotide
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PN US2003077720-A1.
PD 24 APR-2003.
PA (GETH) GENENTECH IN
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RESULT 1306
ID ADC52623 standard; c
DE Novel human secreted
PN US2003087365-A1.
PD 08-MAY-2003.
Query Match
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                                                                                          ADC56977 standard; cDNA; Novel human secreted and US2003087366-A1.
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Novel human secreted
US2003082692-A1.
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15-MAY-2003.
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Human PRO polynucleotide #25.
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ADC89866 standard;

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Best Local Similarity RESULT 1318
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(GETH ) GENENTECH INC.
21.7%; /
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Human PRO polynucleotide
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ADD09151 standard; cDNA; 3719
Human PRO polynucleotide #25.
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Novel human secreted and transmembrane
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Human PRO polynucleotide #25.
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CDNA encoding human PRO polypeptide
US2003194769-A1.
16-OCT-2003.
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ADD92183 standard; cDNA;
Human PRO polynucleotide
US2003199030-A1.
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RESULT 1339
ID ADE21922 standard; c
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Human PRO polynucleotide #25.
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(GETH) GENENTECH INC.
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                    Novel human secreted and transmembrane protein PRO4799 cDNA US2003194767-A1.
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cDNA encoding human PRO polypeptide #25.
US2003207417-A1.
06-NOV-2003.
                  ADD78592 standard; cDNA; 3719 BP.
cDNA encoding human PRO polypeptide #25
US2003203429-A1.
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(GETH ) GENENTECH INC.
21.7%;
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Human PRO polynucleotide #25.
US2003199059-A1.
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Human PRO polynucleotide
US2003194768-A1.
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Human PRO polynucleotide
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Human PRO polynucleotide #25.
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(GETH) GENENTECH INC.
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Human PRO polynucleotide #25.
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Human PRO polynucleotide
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16-OCT-2003.
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(GETH ) GENENTECH INC.
(GETH ) 21.7%; 5
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Human PRO polynucleotide #25.
US2003207372-A1.
06-NOV-2003.
(GETH) GENENTECH INC.
(GETH) GENENTECH S0.28; Press Local Similarity 80.28; Pr
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06-NOV-2003.

(GETH ) GENENTECH INC.

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                                           Novel human secreted and transmembrane US2002207388-A1.
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Novel human secreted and transmembrane
US2003207385-A1.
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06-NOV-2003.
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Novel human secreted and transmembrane
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Novel human secreted and
US2003207377-A1.
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Novel human secreted and transmembrane
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Human PRO polynucleotide #25.
US2003211571-A1.
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Human PRO polyrucleotide #25.
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cDNA encoding human PRO polypeptide #25.
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Human PRO polynucleotide #25.
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US2003199029-A1. 
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Novel human secreted and transmembrane protein PRO4799
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US2003207351-A1.
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ID ADG08055 standard; cl
DE Novel human secreted
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RESULT 1415
ID ADG05808 standard; cI
DE Human PRO polynucleot
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Novel human secreted and transmembrane
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                Human PRO polynucleotide US2003207423-A1.
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Best Local Similarity
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PN US:
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16-OCT-2003.
(GETH) GENENTECH INC.
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80.2%;
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06-NOV-2003.
(OETH) GENENTECH INC.
(OETH) 31.7%;
(OETH) 80.2%;
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                                                                                                     ADG57134 standard; cDNA; 3719 BP.
Novel human secreted and transmembrane
US2003207362-A1.
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Human PRO polynucleotide #25.
US2003207358-A1.
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(GETH ) GENENTECH INC.
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                    ADG56582 standard; cDNA; Novel human secreted and US2003207364-A1.
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(GETH) GENENTECH INC.
21.7%;
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Novel human secreted and transmembrane protein PRO4799
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Best Local Similarity
RESULT 1427
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PN US2003207365-A1.
PD 06-NOV-2003.
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Novel human secreted a
US2003207365-A1.
06-NOV-2003.
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(GETH ) GENENTECH INC.
21.7%; (
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(GETH ) GENENTECH INC.
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)6-NOV-2003.

(GETH ) GENENTECH INC.

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                                      Novel human secreted and transmembrane US2003207419-A1.
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Human PRO polynucleotide
US2003077723-A1.
24-APR-2003.
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Human PRO polynucleotide
US2003207805-A1.
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06-NOV-2003.
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Novel human secreted and transmembrane
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Best Local Similarity

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ID ADG61142 standard;
DE Novel human secrete
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06-NOV-2003.
(GETH ) GENENTECH INC.
(GETH ) 21.7%; (21.7%; (21.7%; (21.7%))
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30-JAN-2003.
(GETH ) GENENTECH INC.
(SETH ) GENENTECH 21.7%; /
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16-OCT-2003.
(GETH) GENENTECH INC.
Match 21.79
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16-NOV-2003.
16-ETH ) GENENTECH INC.
21.7%;
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Novel human secreted and
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06-NOV-2003.
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(GETH ) GENENTECH
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BEST LOCAL SIMILARITY
RESULT 1446
ID ADG09581 stand
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PN US2004
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RESULT 1452
ID ADJ77155 standard; c
DE Human PRO polynucleo
PN US2004038336-A1.
PD 26-FEB-2004.
Best Local Similarity
RESULT 1454
ID ADM27413 standard;
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Best Local Similarity
RESULT 1447
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(GETH ) GENENTECH INC.
(31.7%;
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06-NOV-2003.
(GETH ) GENENTECH INC.
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Match 21.7%;
80.2%;
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                                                        cDNA encoding human US2004038335-A1.
                                                                  ADJ65277 standard; cDNA; cDNA encoding human PRO r
                                                                                                                                   Human PRO polynucleotide US2004038336-A1.
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Novel human secreted and transmembrane protein PRO4799
US2004039164_A1.
26-FEB-2004.
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Novel human secreted
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ADM27413 standard; cDNA; 3719

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RESULT 14
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RESULT 1456
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25-MAR-2004.
(GETH ) GENENTECH INC.
(GETH ) GENENTECH 21.7%; {
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US2004048333-A1.
11-MAR-2004.
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22-APR-2004.
(GETH ) GENENTECH INC.
21.7%; ?
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cDNA encoding human PRO polypeptide #25.
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cDNA encoding human PRO polypeptide
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(REAS-) RES ASSOC BIOTECHNOLOGY.

XY Match
21.7%; Sco

20.2%; Pre
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Novel human secreted and transmembrane
US2003207354-A1.
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WO2004028479-A2.
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                                                                             ABA19615 standard; DNA; 4352 BP.
Human nervous system related polynucleotide
WO200159063-A2.
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                                (HUMA-) HUMAN GENOME SCI INC.
ry Match 21.7%;
t Local Similarity 81.4%;
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           ВP
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                                                                                                                                                                          Human glycogen synthase WO200152865-A1.
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YY Match 21.7%;

t Local Similarity 72.4%;
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Human immune/haematopoietic antigen genomic
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Human immune/haematopoietic antigen genomic sequence
WOZ00157182-A2.
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ry Match 21.7%;

t Local Similarity 79.1%;
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09-AUG-2001.
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Human immune/haematopoietic antigen
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                                                                                                                                                                                                                                                                               Human nervous system related polynucleotide SEQ WO200159063-A2
                                                                                                    AAV05384 standard; DNA; 14237
Human cathepsin K gene.
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ry Match 21.7%;
t Local Similarity 76.9%;
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09-AUG-2001.
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AAL07092 standard;
                    (SMIK) SMITHKLINE BEECHAM CORP. (HUMA-) HUMAN GENOME SCI INC. (GENO-) INST GENOMIC RES. (GENO-) INST GENOMIC RES. 21.7%; Sccry Match 21.7%; Scc Local Similarity 81.8%; Pre
                                                                                           WO9747642-A1.
                                                                                                                                                                                                                                                                                                          ABA16395 standard;
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                                                                                                                                                                                                                                                                                                                             ocal Similarity
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antigenic target
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Q ID 386.
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21.7%;
80.2%;
DNA; 14792 BP
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No. 1e-45;
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No.
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No. 1.4e-45;
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No. 1.2e-45;
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No.
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            טא 2;
1.6e-45;
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                                                                                                                                          5.6; DB 4;
1.5e-45;
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10-45;
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.4e-45;
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                                                                                                                                                      Length 12394;
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                                   Length 14237;
                                                                                                                                                                                                                                                  Length 10553;
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Query
Best Loc.
RESULT 1477
ID ACN445'
DE Huma'
PN WO'
PD J'
PA
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Best Local Si
RESULT 1474
ID AAL07093 E
BE Human repi
  Best Local Similarity
RESULT 1481
ID ADE82926 standard;
DE Human FOSB genomic
                                                                                                                                                                                    Best Local Similarity RESULT 1479 ID ADA02449 standard;
                                                                                                                               Query Match
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09-APR-1998.

(RAPP/) RAPPOLD-HOERBRAND G.

(RAPP/) 21.7%;

ery Match 21.7%;

82.6%;
                                                                                                               402003.
17-JUL-2003.
(SAGR-) SAGRES DISCOVERY.
21.7%;
21.7%;
21.7%;
21.7%;
21.7%;
21.7%;
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(HUMA-) HUMAN GENOME SCI INC.
21.7%;
2ry Match 21.7%;
75.1%;
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                                                                         ADB72188 standard;
Human FOSB gene.
WC2003008583-A2.
                                                                                                                                                                                                                                                                                                                           Human genomic sequence hCG38237.
WO2003073826-A2.
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                                                                                                                                                                       ADA02449 standard; DNA; 27184 BP.
Human FOSB carcinoma associated gene,
                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003066869-A1.
 ADE82926 standard;
Human FOSB genomic
                               (SAGR-) SAGRES DISCOVERY.

ry Match 21.7
t Local Similarity 80.2
                                                                  30-JAN-2003
                                                                                                                                                                                                                                        01-MAY-2003
                                                                                                                                                                                                                                                   WO2003035837-A2.
                                                                                                                                                                                                                                                             Human FOSB carcinoma
                                                                                                                                                                                                                                                                      AAD56087 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD58283 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human reproductive system related WO200155320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAL07094 standard;
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ry Match 21.7%;
t Local Similarity 80.2%;
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ry Match 21.7%;
t Local Similarity 82.6%;
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ry Match 21.7%;
t Local Similarity 75.1%;
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TY Match 21.7%; Score 19
Local Similarity 83.1%; Pred. No.
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DNA; 27184 BP.
DNA sequence.
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ma associated (
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                                                                                               DNA; 27184
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21.7%;
75.1%;
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No.
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No. 1.8e-45;
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No. 1.7e-45;
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No.
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5.6; DB 9
1.8e-45;
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                                 .6; DB 1
2.1e-45;
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2.1e-45;
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.6e-45;
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Best Local Similarity
RESULT 1489
ID ACN44594 standard; DI
DE Human genomic sequent
PN W02003073826-A2.
PD 12-SEP-2003.
                                                                                                                                                              Best Local Similarity
RESULT 1488
ID AD052582 standard; D
DE Human kinase genomic
PN US2004101885-A1.
PD 27-MAY-2004.
                              Best Local Similarity
RESULT 1490
                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 1487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 1485
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Best Local Similarity
RESULT 1484
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Best Local Similarity
RESULT 1482
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ADQ97278 standard; DNA; Human cancer associated WO2004060304-A2.
                                                                                   ACN44594 standard; DNA; 74234 BP. Human genomic sequence hCG15373. WO2003073826-A2.
                                                                                                                                                                                                                                                                                                                                           Human calcium/calmodulin-dependent US6387677-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                          Human cancer associated sequence WO2004060304-A2.
                                                                                                                                                                        Human kinase genomic US2004101885-A1.
                                                                                                                                                                                                                                                              Genomic DNA encoding US2002132325-A1.
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Human SHOX (short stature
WO9814568-A1.
09-APR-1998.
                                                                                                                                                                                                                                                                                   ABX10916 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADQ97152 standard; DNA; Human cancer associated
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:ry Match 21.7%;
it Local Similarity 82.6%;
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Human immune/haematopoietic antigen
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                                                                                                                                                                                                                                          (PEKE )
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                                                               SAGRES
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                                         S DISCOVERY.
21.7%;
arity 80.2%;
                                                                                                                                                                                   ; DNA; 62804
nic DNA.
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ng novel human
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stature homeobox
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78.1%;
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80.2%;
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70.6%;
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70.6%;
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80.2%;
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70.6%;
          86149 BP.
sequence
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          HD08-025,
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No. 2.4
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                                         3.1e-45;
                                                                                                                               .6; DB 1
2.9e-45;
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2.9e-45;
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2.9e-45;
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2.8e-45;
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2.1e-45;
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.8e-45;
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.2e-45;
          SEQ
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                                                                                                                                           62804;
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PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.7%; {
Best Local Similarity 80.2%; F
RESULT 1493
ID ADAGRAPA
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Best Local Similarity
RESULT 1495
ID ADM74483 standard; DN
DE Human carcinoma assoc
PN US2004072154-A1.
PD 15-APR-2004.
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PA (SAGR.) SAGRES DISCOVERY INC.

Query Match

Best Local Similarity 82.6%;

RESULT 1491
                                                                                                                             Best Local Similarity RESULT 1500
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Best Local Similarity
RESULT 1498
Query Match
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RESULT 1496
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RESULT 1494
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Best Local Similarity
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Human glycoprotein VI (platelet) (GP6;GPIV;GPVI) genomic DNA.

ery Match
21.7%; Score 196.6; DB 12; Length 944

st Local Similarity 82.6%; Pred. No. 3.3e-45;
                                                                                                                                                                                                                                                                                                                                                                                                   UBbs-2002.
04-JUN-2002.
04-JUN-2002.
(ISIS-) ISIS PHARM INC.
(ISIS-) ISIS PHARM INC.
21.7%;
PATY Match 21.1%;
90.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB72626 standard; DNA; 96594 BP. Human BLM gene. WO2003008583-A2.
                                                                         ADQ18808 standard; DNA; 111084 BP. Human soft tissue sarcoma-upregulated WO2004048938-A2.
                                                                                                                                      11-ARR-2002.

11-ARR-2002.

(GENE-) GENE LOGIC INC.

21.7%;

21.7%;

21.7%;

79.1%;
                                                                                                                                                                                                                       ABN95044 standard; DNA; 110096 BP. Gene #1542 used to diagnose liver cancer. W0200229103-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADM74483 standard; DNA; 96594 BP.
Human carcinoma associated (CA) nucleic acid #76
US2004072154-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUL-2003.
17-JUL-2003.
(SAGR-) SAGRES DISCOVERY.
21.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC85367 standard; DNA; 96593 BP. Mouse Blm coding sequence. WO2003045230-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD41740 standard; DNA; 99500 BP.
Human RECQL2 DNA #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADA02888 standard; DNA; 96594 BP.
(PROT-) PROTEIN DESIGN LABS INC.
ry Match 21.7%; Sco
t Local Similarity 80.2%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MORR/) MORRIS D W.
(ENGE/) ENGELHARD E K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.7%;
80.2%;
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80.2%;
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80.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 196.6; DB 12;
Pred. No. 3.2e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 196.6; DB 10; Pred. No. 3.4e-45;
                                                                                                                                                Score 196.6; DB 6; Length 110096; Pred. No. 3.6e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 196.6; DB 12; Pred. No. 3.4e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 196.6; DB 9; Pred. No. 3.4e-45;
 Score 196.6; DB 12; Pred. No. 3.6e-45;
                                                                                                                                                                                                                                                                                              Score 196.6; DB 12; Pred. No. 3.6e-45;
                                                                                                                                                                                                                                                                                                                                                    Score 196.6; DB 9;
Pred. No. 3.6e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 196.6; DB 10;
Pred. No. 3.4e-45;
                                                                                                                                                                                                                                                                                                                                                                                                            Score 196.6; DB 6; Pred. No. 3.4e-45;
                                                                                            DNA -
                                                                                            SEQ
                                                                                            ID
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 99500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 96594;
                                                                                                                                                                                                                                                                                                                                                                        Length 110000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 94400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 86149;
                 Length 111084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 96594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 96594;
                                                                                                                                                                                                                                                                                                                  Length 110000;
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